

STIC-Biotech/ChemLib

80853

From: Winkler, Ulrike
Sent: Thursday, November 21, 2002 3:20 PM
T : STIC-Biotech/ChemLib

STIC,
Please search SEQ ID 48 and 51 of application 09/670105 please limit the search results to oligos that are 50 nt or less.

Thanks, Ulrike

Ulrike Winkler, Ph.D.
Patent Examiner
Crystal Mall 1, 8D09 ✓
1911 South Clark Place
Arlington, VA 22202
tel. 703-308-8294
fax. 703-308-4426

SEK

Mary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155

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NOV 21 2002
STIC

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 12/6/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

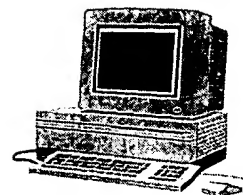
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BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, **CM1-1E01** or e-mail **mary.hale@uspto.gov**.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 5, 2002, 22:51:23 : Search time 1611.47 Seconds
(without alignments)
261.304 Million cell updates/sec

Title: US-09-670-105-51
Perfect score: 26
Sequence: 1 GTGCTTCGTCTGCTCCAGAACCC 26
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 16154066 seqs, 8097743376 residues
Word size : 0
Total number of hits satisfying chosen parameters: 102860
Minimum DB seq length: 0
Maximum DB seq length: 50
Post-processing: Listing first 45 summaries

Database : EST:*

- 1: em_estba:**
- 2: em_esthum:**
- 3: em_estin:**
- 4: em_estmu:**
- 5: em_estov:**
- 6: em_estpl:**
- 7: em_estro:**
- 8: em_estl:**
- 9: gb_est1:**
- 10: gb_est2:**
- 11: gb_hlc:**
- 12: gb_est3:**
- 13: gb_est4:**
- 14: gb_est5:**
- 15: em_estfun:**
- 16: em_estom:**
- 17: gb_gss:**
- 18: em_gss_hum:**
- 19: em_gss_inv:**
- 20: em_gss_pln:**
- 21: em_gss_vrt:**
- 22: em_gss_fun:**
- 23: em_gss_mam:**
- 24: em_gss_mus:**
- 25: em_gss_Other:**
- 26: em_gss_pro:**
- 27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	12	46.2	30 17 AZ487397
2	12	46.2	42 17 AZ602471
3	12	46.2	46 9 A1581188
4	11	42.3	22 17 TAI14G12Q
5	11	42.3	29 17 TA36B10P
6	11	42.3	30 12 BG400161

1	12	46.2	30 17 AZ487397
2	12	46.2	42 17 AZ602471
3	12	46.2	46 9 A1581188
4	11	42.3	22 17 TAI14G12Q
5	11	42.3	29 17 TA36B10P
6	11	42.3	30 12 BG400161

c	7	11	42.3	32	13	BI192552
c	8	11	42.3	32	17	AZ988809
c	9	11	42.3	34	13	AJ001219
c	10	11	42.3	37	9	AI077338
c	11	11	42.3	37	10	AW698830
c	12	11	42.3	40	9	AI159139
c	13	11	42.3	40	9	AI159650
c	14	11	42.3	40	17	AZ832139
c	15	11	42.3	41	17	AZ626793
c	16	11	42.3	43	17	BH847687
c	17	11	42.3	44	9	AA922988
c	18	11	42.3	47	17	AZ795746
c	19	11	42.3	50	9	AU106106
c	20	11	42.3	50	9	AU106123
c	21	11	42.3	50	9	AU106124
c	22	11	42.3	50	9	AU106147
c	23	11	42.3	50	9	AU106150
c	24	11	42.3	50	9	AU106157
c	25	11	42.3	50	9	AU106179
c	26	11	42.3	50	9	AU106180
c	27	11	42.3	50	9	AU106204
c	28	11	42.3	50	9	AU106244
c	29	11	42.3	50	9	AU106246
c	30	11	42.3	50	9	AU106247
c	31	11	42.3	50	9	AU106248
c	32	10	38.5	19	17	AZ500630
c	33	10	38.5	20	17	AZ368205
c	34	10	38.5	24	17	AZ781101
c	35	10	38.5	24	17	TA306E03P
c	36	10	38.5	27	17	AZ483323
c	37	10	38.5	28	9	AA978158
c	38	10	38.5	29	9	AU258464
c	39	10	38.5	29	17	AZ310013
c	40	10	38.5	29	17	TA330A07P
c	41	10	38.5	31	10	AV833478
c	42	10	38.5	33	17	AZ489566
c	43	10	38.5	33	17	AZ781782
c	44	10	38.5	35	17	BH851755
c	45	10	38.5	35	17	TA275C03P

ALIGNMENTS

RESULT 1	AZ487397	AZ487397	30 bp	DNA	linear	GSS 05-OCT-2000
LOCUS	LM0317J04F	Mouse 10kb plasmid	UUGC1M	library	Mus musculus	genomic
DEFINITION	clone UUGC1M0317J04 F, DNA sequence.					
ACCESSION	AZ487397					
VERSION	AZ487397.1	GI:10655101				
KEYWORDS	GSS.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.					
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.					
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00					

Plate: 0317 row: J column: 04
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers
 1. .30

FEATURES

source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0317J04"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 8 a 8 c 2 g 12 t
 ORIGIN
 Query Match 46.2%; Score 12; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CTTCTCTGCTGCT 15
 Db 5 CTTCTCTGCTGCT 16
 |||||
 |||||

RESULT 2

AZ602471/c
 LOCUS
 DEFINITION
 1M0421D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0421D16 F. DNA sequence.

ACCESSION
 AZ602471
 VERSION
 AZ602471.1 GI:11724661

KEYWORDS
 GSS.

SOURCE
 house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 42)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0421 row: D column: 16
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 42.
 Location/Qualifiers
 1. .42

FEATURES

source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0421D16"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 8 a 7 c 15 g 12 t
 ORIGIN
 Query Match 46.2%; Score 12; DB 17; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TCCCAAGAACCC 26
 Db 33 TCCCAAGAACCC 22
 |||||
 |||||

RESULT 3

AI581188/c
 LOCUS
 DEFINITION
 t194g04.x1 NCI_CGAP_Col4 Homo sapiens cDNA clone IMAGE:2134774 3.
 similar to WP:CI7E4.7 CE08256 EXTENSIN LIKE ;contains MER30.b1 TARI
 repetitive element ;, mRNA sequence.

ACCESSION
 AI581188
 VERSION
 AI581188.1 GI:4565564

KEYWORDS
 EST.

SOURCE
 human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 46)

AUTHORS
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
 Unpublished (1997)

COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 829 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1
 POLYA=No.

FEATURES

Location/Qualifiers

1..46
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2154774"
 /clone_lib="NCL_CGAP_Col4"
 /tissue_type="moderately-differentiated adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site.1: SalI;
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.7 kb. Life Technologies catalog #:
 11531-019"

BASE COUNT 26 a 2 c 12 g 6 t

ORIGIN

Query Match 46.2%; Score 12; DB 9; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TCCCAAGAACCC 26
 |||||
 Db 16 TCCCAAGAACCC 5

RESULT 4

TAIL4G120/c

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 114g12, reverse sequence,
 genomic survey sequence.

ACCESSION AL462979

VERSION AL462979.1 GI:11832660

KEYWORDS GSS.

SOURCE Trypanosoma brucei.

ORGANISM

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 22)

REFERENCE
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

DIRECT SUBMISSION

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..22
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="114g12"

BASE COUNT 6 a 5 c 7 g 4 t

ORIGIN

Query Match 42.3%; Score 11; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.3e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTTCCTGC 11
 |||||
 Db 21 GTGCTTCCTGC 11

RESULT 5

TA36B10P

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 36b10, forward sequence,
 genomic survey sequence.

ACCESSION AL453638

VERSION AL453638.1 GI:11854781

KEYWORDS GSS.

SOURCE Trypanosoma brucei.

ORGANISM

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 29)

REFERENCE
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

DIRECT SUBMISSION

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..29
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="36b10"

BASE COUNT 6 a 8 c 8 g 7 t

ORIGIN

Query Match 42.3%; Score 11; DB 17; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTCCTGCTGCT 15

|||||

Db 3 TTCCTGCTGCT 13

RESULT 6

BG400161/c

LOCUS

DEFINITION 602440944F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4556602 5',
 mRNA sequence.

ACCESSION BG400161

VERSION BG400161.1 GI:13293609

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 30)

AUTHORS

TITLE

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCMI259 row: h column: 11
High quality sequence stop: 24.
Location/Qualifiers
1. .30

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4556602"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgcctcgcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCCGACATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
10 a 5 c 12 g 3 t

BASE COUNT
ORIGIN

Query Match 42.3%; Score 11; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCCTGCTGTC 16

Db 11 TCCTGCTGTC 1

RESULT 7

BI192552/c
LOCUS
DEFINITION
602945447F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:5088947 5', mRNA sequence.
ACCESSION
BI192552
VERSION
BI192552.1 GI:14647572
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCMI848 row: m column: 12
High quality sequence stop: 32.
Location/Qualifiers
1. .32

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5088947"

/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. 1"
6 a 6 c 17 g 3 t

Query Match 42.3%; Score 11; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGCTGCTCC 18

Db 23 CTGCTGCTCC 13

RESULT 8

AZ988809

LOCUS

DEFINITION
2M0271N21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0271N21 R, DNA sequence.

ACCESSION

AZ988809

VERSION

AZ988809.1 GI:13860036

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 32)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0271 row: N column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers
1. .32

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0271N21"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl1473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 42.3%; Score 11; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCTCTGCTGCTC 16
|||||

Db 5 TCTCTGCTGCTC 15

RESULT 9

BJ001219/c

LOCUS

DEFINITION BJ001219 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA004B08 5',
mRNA sequence.

ACCESSION BJ001219

VERSION BJ001219.1 GI:17361486

KEYWORDS EST.

SOURCE Japanese medaka.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.

REFERENCE 1 (bases 1 to 34)

Kohara.Y., Shin-I.T., Kimura.T., Narita.T., Jindo.T. and Takeda.H.
Medaka EST Project in Takeda's lab
Unpublished (2001)

CONTACT Tadasu Shin-i

CENTER For Genetic Resource Information

NATIONAL Institute of Genetics

111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

FEATURES

source

1..34
/organism="Oryzias latipes"
/strain="Hd-r"
/db_xref="taxon:8090"
/clone="MF01SSA004B08"
/clone_lib="MF01SSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
13 a 5 c 12 g 4 t

BASE COUNT

ORIGIN

Query Match 42.3%; Score 11; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTCTCTGCTGCT 15
|||||

Db 30 TTCTCTGCTGCT 20

RESULT 10

AI077338

LOCUS

DEFINITION

AI077338 37 bp mRNA linear EST 24-SEP-1998
OY65g02.x1 NCLCGAP CLL1 Homo sapiens cDNA clone IMAGE:1670738 3',
similar to TR.Q64657 Q64657 INTEGRIN BETA 5 SUBUNIT ;, mRNA
sequence.

ACCESSION AI077338

VERSION AI077338.1 GI:3411746

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 37)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html

Trace considered overall poor quality

Insert Length: 1168 Std Error: 0.00

Seq primer: -40ml3 fwd. Et from Amersham

High quality sequence stop: 1.

FEATURES

source

1..37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1670738"
/clone_lib="NCI-CGAP CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAAGTGGAGCGCGCATTCGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT733 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 18 a 12 c 7 g 0 t

ORIGIN

Query Match 42.3%; Score 11; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCCAAGAACCC 26
|||||

Db 6 CCCAAGAACCC 16

RESULT 11

AW698830

LOCUS

DEFINITION AW698830 37 bp mRNA linear EST 17-APR-2000
r438 non-glandular-haired subtracted cDNA library Medicago sativa
cDNA, mRNA sequence.

ACCESSION AW698830

VERSION AW698830.1 GI:7581416

KEYWORDS EST.

SOURCE Medicago sativa.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

/clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"

/note=Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
 Site_2: DraIII (CACTATGTG); 1st strand cDNA was primed
 with an oligo(dT) primer (ATGGGCTTTTTTTTTTTTTT);
 double-stranded cDNA was ligated to a DraIII adaptor
 [TGTGGCCCTACTGG], digested and cloned into distinct DraIII
 sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
 CACTATGTG). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).
 Custom primers for sequencing: 5' end primer
 CTTCTGCTCTAAAGCTGCG and 3' end primer
 CGACCTGCACCTCGAGCACA."

BASE COUNT 14 a 11 c 9 g 6 t
 ORIGIN

Query Match 42.3%; Score 11; DB 9; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGCTGCTCCC 18
 |||||
 Db 21 CTGCTGCTCCC 11

RESULT 14

A2832139

LOCUS

DEFINITION 2M0112P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0112P14 F, DNA sequence.

ACCESSION A2832139

VERSION A2832139.1

KEYWORDS GI:13002047

SOURCE GSS.

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: P Column: 14

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

1. 40

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0112P14"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note=Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (g11473211419b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells.
 and selected for ampicillin resistance."

BASE COUNT 5 a 11 c 10 g 14 t
 ORIGIN

Query Match 42.3%; Score 11; DB 17; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTCTCTGCTGCT 15
 |||||
 Db 21 TTCTCTGCTGCT 31

RESULT 15

A2626793/c

LOCUS

DEFINITION 1M0467D15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0467D15 F, DNA sequence.

ACCESSION A2626793

VERSION A2626793.1

KEYWORDS GI:11748983

SOURCE GSS.

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 41)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0467 row: D Column: 15

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

1. 41

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0467D15"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note=Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 12 c 8 g 8 t
ORIGIN
Query Match 42.3%; Score 11; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CTGCTCCCAAG 21
|||||
Db 31 CTGCTCCCAAG 21

Search completed: December 6, 2002, 00:45:10
Job time : 1613.47 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 20:34:23 ; Search time 48.8163 Seconds
(without alignments)
163.339 Million cell updates/sec

Title: US-09-670-105-51

Perfect score: 26

Sequence: 1 GTGCTTCCTGCTGCTCCCAAGACC 26

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	4	US-09-092-077-51
2	26	100.0	26	4	US-09-092-077-52
3	26	100.0	27	2	US-08-442-010-6
4	23	88.5	24	4	US-09-481-288-23
5	21	80.8	38	4	US-08-679-493A-32
6	20	76.9	24	1	US-08-470-202-34
7	20	76.9	24	1	US-08-471-770-34
8	20	76.9	24	2	US-08-468-059-34
9	20	76.9	24	4	US-09-109-916-34
10	19	73.1	36	1	US-08-472-756-5
11	19	73.1	36	2	US-08-610-955-5
12	18	69.2	18	1	US-08-472-756-2
13	18	69.2	18	2	US-08-610-955-2
14	18	69.2	40	1	US-08-470-202-27
15	18	69.2	40	1	US-08-471-770-27
16	18	69.2	40	1	US-08-472-756-3
17	18	69.2	40	2	US-08-468-059-27
18	18	69.2	40	2	US-08-610-955-3
19	18	69.2	40	4	US-09-109-916-27
20	17	65.4	39	3	US-08-889-841B-49
21	15	57.7	20	1	US-08-470-202-21
22	15	57.7	20	1	US-08-470-202-35
23	15	57.7	20	1	US-08-471-770-21
24	15	57.7	20	1	US-08-471-770-35
25	15	57.7	20	1	US-08-468-059-21
26	15	57.7	20	2	US-08-468-059-35
27	15	57.7	20	2	US-08-628-687-2

c 28	15	57.7	20	3	US-08-388-353-619	Sequence 619, App
c 29	15	57.7	20	3	US-08-488-551B-619	Sequence 619, App
c 30	15	57.7	20	4	US-09-109-916-21	Sequence 21, Appl
c 31	15	57.7	20	4	US-09-109-916-35	Sequence 35, Appl
32	14	53.8	20	2	US-08-227-180B-37	Sequence 37, Appl
33	13	50.0	18	1	US-08-363-240A-1121	Sequence 1121, Ap
34	12	46.2	15	1	US-08-363-240A-226	Sequence 226, App
35	12	46.2	20	2	US-08-227-180B-36	Sequence 36, Appl
36	12	46.2	20	2	US-09-580-189-5	Sequence 5, Appl
37	12	46.2	22	3	US-08-738-000-12	Sequence 12, Appl
38	12	46.2	22	4	US-09-258-928-12	Sequence 12, Appl
c 39	12	46.2	22	4	US-09-656-952-4	Sequence 4, Appl
40	12	46.2	34	4	US-08-469-260A-616	Sequence 616, App
c 41	12	46.2	37	4	US-08-469-260A-615	Sequence 615, App
42	12	46.2	39	2	US-08-834-655-15	Sequence 15, Appl
43	12	46.2	39	3	US-09-363-574-15	Sequence 15, Appl
44	12	46.2	39	4	US-09-363-526-15	Sequence 15, Appl
c 45	12	46.2	40	1	US-08-361-920-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-09-092-077-51
; Sequence 51, Application US/09092077
; Patent No. 6194142

GENERAL INFORMATION:

APPLICANT: Moncany, Maurice
APPLICANT: Montagnier, Luc
TITLE OF INVENTION: Nucleotide Sequences Derived From The
TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type.
TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis
TITLE OF INVENTION: Of The Diseases Due To Those Viruses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/092.077

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/472.928

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/160,465

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8912371

FILING DATE: 20-SEP-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8907354

FILING DATE: 06-FEB-1989

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 02356.0062-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

```
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-092-077-51

Query Match      100.0%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTTCCTGCTGCTCCCAAGAACCC 26
Db 1 GTGCTTCCTGCTGCTCCCAAGAACCC 26

RESULT 2
US-09-092-077-52/c
; Sequence 52, Application US/09092077
; Patent No. 6194142
; GENERAL INFORMATION:
; APPLICANT: Moncany, Maurice
; APPLICANT: Montanier, Luc
; TITLE OF INVENTION: Nucleotide Sequences Derived From The
; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis
; TITLE OF INVENTION: Of The Diseases Due To Those Viruses
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,077
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,928
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/160,465
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 8912371
; FILING DATE: 20-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 8907354
; FILING DATE: 06-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0062-02000
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-092-077-52
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Query Match      100.0%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTTCCTGCTGCTCCCAAGAACCC 26
Db 26 GTGCTTCCTGCTGCTCCCAAGAACCC 1

RESULT 3
US-08-442-010-6
; Sequence 6, Application US/08442010
; Patent No. 5849994
; GENERAL INFORMATION:
; APPLICANT: NARAYAN, Opendra
; TITLE OF INVENTION: Animal Model for HIV-1 Induced Disease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,010
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,645
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR primer"
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..27
; OTHER INFORMATION: /note= "complementary to HX8c2"
; OTHER INFORMATION: (gpl20) 7810-7784"
US-08-442-010-6

Query Match      100.0%; Score 26; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTTCCTGCTGCTCCCAAGAACCC 26
Db 2 GTGCTTCCTGCTGCTCCCAAGAACCC 27

RESULT 4
US-09-481-288-23/c
; Sequence 23, Application US/09481288
; Patent No. 6235504
; GENERAL INFORMATION:
; APPLICANT: Zhang, Linqi
; APPLICANT: Lewin, Sharon R
; APPLICANT: Kostrikis, Leonidios
```

```
; APPLICANT: Ho, David D
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENOMIC EQUIVALENT MARKERS AND
; TITLE OF INVENTION: THEIR USE IN QUANTITATING CELLS AND POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES THEREIN
; FILE REFERENCE: 2378-1-001N
; CURRENT APPLICATION NUMBER: US/09/481.288
; CURRENT FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PRIMER
US-09-481-288-23

Query Match      88.5%; Score 23; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTTCCTGCTGCTCCCAAGAA 23
    |||||||
Db 23 GTGCTTCCTGCTGCTCCCAAGAA 1

RESULT 5
US-08-679-493A-32/c
; Sequence 32, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679.493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Human immunodeficiency virus type 1
US-08-679-493A-32

Query Match      80.8%; Score 21; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCCTGCTGCTCCCAAGAACCC 26
    |||||||
Db 38 TCCTGCTGCTCCCAAGAACCC 18

RESULT 6
US-08-470-202-34
; Sequence 34, Application US/08470202
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
```

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; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.202
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132.653
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael J. Blake
; REGISTRATION NUMBER: 37,096
; REFERENCE/DOCKET NUMBER: 05495-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-470-202-34

Query Match      76.9%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCTGCTGCTCCCAAGAACCC 26
    |||||||
Db 1 CCTGCTGCTCCCAAGAACCC 20

RESULT 7
US-08-471-770-34
; Sequence 34, Application US/08471770
; Patent No. 5770427
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
```

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;
;
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,770
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Carol P. Einaudi
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 05495-0001-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 34:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-471-770-34

Query Match 76.9%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTGCTGCTCCCAAGAACCC 26
Db 1 CCTGCTGCTCCCAAGAACCC 20

RESULT 8
US-08-468-059-34
; Sequence 34, Application US/08468059
; Patent No. 5840480
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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;
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,059
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Carol P. Einaudi
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 05495-0001-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 34:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-468-059-34

Query Match 76.9%; Score 20; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTGCTGCTCCCAAGAACCC 26
Db 1 CCTGCTGCTCCCAAGAACCC 20

RESULT 9
US-09-109-916-34
; Sequence 34, Application US/09109916
; Patent No. 627561
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495-0001-04
; CURRENT APPLICATION NUMBER: US/09/109,916
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: DE P 42 33 646.5
; EARLIER FILING DATE: 1992-10-06
; EARLIER APPLICATION NUMBER: DE P 42 35 718.7
; EARLIER FILING DATE: 1992-10-22
; EARLIER APPLICATION NUMBER: DE P 42 44 541.8
; EARLIER FILING DATE: 1992-12-30
; EARLIER APPLICATION NUMBER: DE P 43 18 186.4
; EARLIER FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 34
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-109-916-34

Query Match 76.9% Score 20; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCTGCTGCTCCCAAGACCC 26
Db 1 CCTGCTGCTCCCAAGACCC 20

RESULT 10
US-08-472-756-5
; Sequence 5, Application US/08472756
; Patent No. 5780227
; GENERAL INFORMATION:
; APPLICANT: SHERIDAN, PATRICK J.
; APPLICANT: GAGNE, JULIO C.
; APPLICANT: ANDERSON, MARY L.
; APPLICANT: LUDTKE, DOUGLAS N.
; TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
; TITLE OF INVENTION: ENZYME INHIBITION ASSAY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472.756
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN ESQ., KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 1014.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-472-756-5

Query Match 73.1% Score 19; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTCCTGCTGCTCCCAAGAA 23
Db 18 TTCCTGCTGCTCCCAAGAA 36

Query Match 73.1% Score 19; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTCCTGCTGCTCCCAAGAA 23
Db 18 TTCCTGCTGCTCCCAAGAA 36

RESULT 11
US-08-610-955-5
; Sequence 5, Application US/08610955

; Patent No. 5853974
; GENERAL INFORMATION:
; APPLICANT: SHERIDAN, PATRICK J.
; APPLICANT: GAGNE, JULIO C.
; APPLICANT: ANDERSON, MARY L.
; APPLICANT: LUDTKE, DOUGLAS N.
; TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
; TITLE OF INVENTION: ENZYME INHIBITION ASSAY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/610.955
; FILING DATE: 05-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472.756
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN ESQ., KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 1014.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-610-955-5

Query Match 73.1% Score 19; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTCCTGCTGCTCCCAAGAA 23
Db 18 TTCCTGCTGCTCCCAAGAA 36

RESULT 12
US-08-472-756-2
; Sequence 2, Application US/08472756
; Patent No. 5780227
; GENERAL INFORMATION:
; APPLICANT: SHERIDAN, PATRICK J.
; APPLICANT: GAGNE, JULIO C.
; APPLICANT: ANDERSON, MARY L.
; APPLICANT: LUDTKE, DOUGLAS N.
; TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
; TITLE OF INVENTION: ENZYME INHIBITION ASSAY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94608
; COMPUTER READABLE FORM:

Query Match 73.1% Score 19; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTCCTGCTGCTCCCAAGAA 23
Db 18 TTCCTGCTGCTCCCAAGAA 36

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/472,756
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GOLDMAN ESQ., KENNETH M.
;; REGISTRATION NUMBER: 34,174
;; REFERENCE/DOCKET NUMBER: 1014.001
;; TELEPHONE: (510) 601-2719
;; TELEFAX: (510) 655-3542
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-472-756-2

Query Match 69.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCCTGCTGCTCCCAAGAA 23
DB 1 TCCTGCTGCTCCCAAGAA 18

RESULT 13
US-08-610-955-2
; Sequence 2, Application US/08610955
; Patent No. 5853974
; GENERAL INFORMATION:
; APPLICANT: SHERIDAN, PATRICK J.
; APPLICANT: GAGNE, JULIO C.
; APPLICANT: ANDERSON, MARY L.
; APPLICANT: LUTYKE, DOUGLAS N.
; TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES BY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/610,955
; FILING DATE: 05-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472,756
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN ESQ., KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 1014.001
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-610-955-2

Query Match 69.2%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCCTGCTGCTCCCAAGAA 23
DB 1 TCCTGCTGCTCCCAAGAA 18

RESULT 14
US-08-470-202-27
; Sequence 27, Application US/08470202
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,202
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael J. Blake
; REGISTRATION NUMBER: 37,096
; REFERENCE/DOCKET NUMBER: 05495-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
US-08-470-202-27

Query Match 69.2%; Score 18; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGCTGCTCCCAAGAACCC 26
|||||
Db 19 TGCTGCTCCCAAGAACCC 36

RESULT 15

US-08-471-770-27
; Sequence 27, Application US/08471770
; Patent No. 5770427

; GENERAL INFORMATION:

; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,770

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/132,653

; FILING DATE: 05-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 33 646.5

; FILING DATE: 06-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 35 718.7

; FILING DATE: 22-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 44 541.8

; FILING DATE: 30-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 43 18 186.4

; FILING DATE: 01-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Carol P. Elnaudi

; REGISTRATION NUMBER: 32,220

; REFERENCE/DOCKET NUMBER: 05495-0001-03000

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-471-770-27

Query Match 69.2%; Score 18; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGCTGCTCCCAAGAACCC 26
|||||
Db 19 TGCTGCTCCCAAGAACCC 36

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Job time : 49.8163 secs

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OM nucleic - nucleic search, using sw model

Run On: December 5, 2002, 21:44:53 : Search time 232.408 Seconds
(without alignments)
251.936 Million cell updates/sec

Title: US-09-670-105-51

Perfect score: 26

Sequence: 1 GTGCTTCTGCTGCTCCCAAGAACCC 26

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

1:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	11 AAQ06938	MMY8 nucleotide co
c 2	26	100.0	26	11 AAQ06939	MMY8bis nucleotide
3	26	100.0	26	18 AAT98046	Human or simian im
c 4	26	100.0	26	18 AAT98047	Human or simian im
5	26	100.0	27	20 AAV08911	PCR primer for SIV
6	26	100.0	30	16 AAQ81321	Human immunodefici
7	26	100.0	30	17 AAT35934	HIV env PCR primer
c 8	26	100.0	34	20 AAX25184	HIV-1 group O gp41
c 9	23	88.5	24	22 AAD07432	HIV-1 env gene amp

10	23	88.5	25	20	AAZ10963	PCR primer for HIV
11	22	84.6	28	14	AAQ40104	RRE Oligonucleotide
12	21	80.8	29	19	AAV20501	Primer ED12 for HI
c 13	21	80.8	38	24	ABA01298	Pseudoknot oligonu
14	20	76.9	24	15	AAQ58958	env d primer. Syn
15	20	76.9	24	20	AAQ22363	HIV-2 PCR primer e
16	19	73.1	36	18	AAT74060	Label extender bla
17	18	69.2	18	18	AAT74057	HIV Rev response e
18	18	69.2	40	15	AAQ58951	3v3longdegi primer
c 19	18	69.2	40	18	AAT74058	Capture extender p
20	18	69.2	40	20	AAQ22352	HIV-1 PCR primer 3
c 21	17	65.4	21	24	ABK65874	Human immunodefici
c 22	17	65.4	28	21	AAW76123	PCR primer GP40F1.
23	17	65.4	39	19	AAV00536	HIV-1 gp120 DNA pr
c 24	15	57.7	20	14	AAQ38852	Sequence of primer
c 25	15	57.7	20	14	AAQ50103	PCR primer used in
c 26	15	57.7	20	15	AAQ58959	HIV primer 1. Syn
c 27	15	57.7	20	15	AAQ58945	SK68 primer. Synt
c 28	15	57.7	20	16	AAQ90020	PCR primer SK 68 d
c 29	15	57.7	20	17	AAT39821	Primer SK68 for HI
c 30	15	57.7	20	17	AAT39821	G3PDH primer for a
c 31	15	57.7	20	20	AAZ23104	HIV-1 gp41 env gen
c 32	15	57.7	20	20	AAQ223791	HIV isolate MVP-51
c 33	15	57.7	20	20	AAQ22364	HIV-1 PCR primer s
c 34	14	53.8	16	17	AAT32681	Ineffective anti-H
35	14	53.8	20	12	AAQ14985	Oligonucleotide #1
36	14	53.8	20	16	AAQ98006	Peptide nucleic ac
37	14	53.8	20	24	ABK65879	Human immunodefici
38	14	53.8	50	22	AAH20074	HERV-W envelope pr
39	13	50.0	18	17	AAT50638	Human CERP hairpin
c 40	13	50.0	21	24	ABN88780	Dombrock carrier m
c 41	13	50.0	22	21	AAA66386	Dog genomic marker
c 42	13	50.0	24	15	AAQ57316	Enzymatic RNA mole
c 43	13	50.0	28	24	ABK69683	Human WTL truncati
c 44	13	50.0	30	24	ABN88719	Dombrock (a) antig
45	13	50.0	30	24	ABN88751	Dombrock (b) antig

ALIGNMENTS

RESULT 1
AAQ06938
ID AAQ06938 standard; DNA; 26 BP.
XX AAQ06938;
AC AAQ06938;
XX
DT 05-MAR-1991 (first entry)
DE MMY8 nucleotide constituent of env gene of HIV-1 Bru, HIV-1 Mal
DE and HIV-1 Eli.
XX HIV-1; AIDS; anti-sense nucleotide; ss.
KW HIV-1; AIDS; anti-sense nucleotide; ss.
XX EP403333-A.
XX
XX
PD 19-DEC-1990.
XX
PF 05-JUN-1990; 90EP-0401520.
XX
XX 20-SEP-1989; 89FR-0012371.
XX
XX (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE RE.

Moncany M, Montagnier L;

WPI; 1990-378039/51.

New nucleotide sequences derived from genome of HIV-1, HIV-2 and
SIV - useful as primers for amplification of immuno-deficiency
PT viruses in diagnosis and for raising antibodies in treatment of
PT HIV infections

OS Synthetic.
OS Human immunodeficiency virus.
OS Simian immunodeficiency virus.
XX
PN EP806484-A2.
XX
PD 12-NOV-1997.
XX
XX 05-JUN-1990; 90EP-0401520.
XX
XX 20-SEP-1989; 89FR-0012371.
PR
XX 02-JUN-1989; 89FR-0007354.
XX
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP) INST PASTEUR.
XX
PI Moncan y M, Montagnier L;
XX
XX WPI; 1997-538622/50.
XX
XX Oligo-nucleotide primers for amplifying retroviral nucleic acids -
PT comprising conserved sequences of human immunodeficiency virus and
PT simian immunodeficiency virus genes
XX
PS Disclosure; Page 8; 23pp; French.
XX
XX The oligonucleotides AAT98010-T98059 are useful as primers for nucleic
CC acid amplification of conserved sequences of the gag, vpr, pol or vpu
CC genes of the HIV-1 strains Bru, Mai, Eli, HIV-2 ROD or simian
CC immunodeficiency virus (SIV) MAC or the nef2, vif2 or vpx genes of HIV-2
CC ROD and SIV MAC. This primer is targetted to sequences in the env gene of
CC the viral strains. The sequences are therefore used to detect HIV-1,
CC HIV-2 or SIV infections.
XX
XX Sequence 26 BP; 6 A; 5 C; 11 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 26; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTTCTGCTGCTCCCAAGAACCC 26
DB 26 GTGCTTCTGCTGCTCCCAAGAACCC 1
RESULT 5
AAV08911
ID AAV08911 standard; DNA; 27 BP.
XX
XX AAV08911;
AC
XX 26-FEB-1999 (first entry)
DT
XX PCR primer for SIV gp120 gene.
DE
XX PCR primer; SIV; gp120 gene; gag gene; chimeric virus; SIV-HIV virus;
KW AIDS-associated symptom; HIV; env protein; ss.
XX
OS Synthetic.
OS Simian immunodeficiency virus.
XX
XX US5849994-A.
PN
XX 15-DEC-1998.
PD
XX 16-MAY-1995; 95US-0442010.
PF
XX 16-MAY-1995; 95US-0442010.
PR
XX (UNIV) UNIV KANSAS MEDICAL CENT.
PA
XX Narayan O;
PI
XX

DR WPI; 1999-069838/06.
XX Chimeric SIV-HIV virus - for producing AIDS symptoms in macaque
PT monkeys
XX
XX Example; Column 13; 13pp; English.
PS
XX This sequence represents a PCR primer for the simian immunodeficiency
CC virus (SIV) gp120 gene. The amplified sequence can be used in the
CC chimeric virus of the invention. The chimeric virus is a chimeric SIV-HIV
CC virus (SHIV) that infects macaque monkeys and causes them to develop
CC AIDS-associated symptoms within 32 weeks, where the virus is generated by
CC at least two passages of a SHIV containing DNA encoding HIV env protein
CC through macaque bone marrow in vivo. The monkeys are useful as an animal
CC model for HIV-1-induced disease.
XX
XX Sequence 27 BP; 5 A; 11 C; 5 G; 6 T; 0 other;
SQ
Query Match 100.0%; Score 26; DB 20; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTTCTGCTGCTCCCAAGAACCC 26
DB 2 GTGCTTCTGCTGCTCCCAAGAACCC 27
RESULT 6
AAQ81321
ID AAQ81321 standard; DNA; 30 BP.
XX
XX AAQ81321;
AC
XX 22-SEP-1995 (first entry)
DT
XX Human immunodeficiency virus-1-HXB2 genome PCR primer ED12.
DE
XX Human immunodeficiency virus type 1; HIV-1; HXB2 genome;
KW PCR primer ED12; heteroduplex mobility assay; ss.
XX
XX Synthetic.
OS
XX WO9501453-A.
PN
XX 12-JAN-1995.
PD
XX 30-JUN-1994; 94WO-US07416.
PF
XX 01-JUL-1993; 93US-0087010.
PR
XX 11-MAY-1994; 94US-0241373.
PR
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Delwart EL, Mullins JI;
PI
XX WPI; 1995-061016/08.
DR
XX Heteroduplex mobility assay for the analysis of nucleic acid
PT sequence diversity - used to analyse sequence variation between
PT genetic loci, and sequence diversity over time in samples
PT serially obtd. from a single source
XX
XX Example 1; Page 60; 83pp; English.
PS
XX AAQ81320 and AAQ81321 (or AAQ81326) are a pair of primers for the first
CC round PCR amplification of the human immunodeficiency virus-1-HXB2
CC genome. The primers were used in a heteroduplex mobility assay, to
CC evaluate intra- and interpatient HIV sequence diversity.
XX
XX Sequence 30 BP; 7 A; 11 C; 6 G; 6 T; 0 other;
SQ
Query Match 100.0%; Score 26; DB 16; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTTCTGCTGCTCCCAAGAACCC 26
|||||
Db 2 GTGCTTCTGCTGCTCCCAAGAACCC 27

RESULT 7

AAT35934
ID AAT35934 standard; DNA; 30 BP.

AC AAT35934;

XX 25-FEB-1997 (first entry)

XX HIV env PCR primer ED12.

XX Rev response element; RRE; silent mutation; immunisation construct;
KW mucosal response; transfection; lipospermine; lipospermidine; DOGS;
KW dioctadecylamidoglycylspermine; polymerase chain reaction; ss.

XX Synthetic.

XX WO9621356-A1.

XX 18-JUL-1996.

XX 03-JUL-1995; 95WO-US08374.

XX 13-JAN-1995; 95US-0372429.

XX (UYVA-) UNIV VANDERBILT.

XX Mitchell WM;

XX WPI; 1996-341965/34.

XX Inducing mucosal immune response by admin. of antigen-encoding DNA
PT - complexed to lipo:spermine or lipo:spermidine, partic. for
PT vaccination against HIV

XX Example; Page 50; 82pp; English.

XX Inducing a mucosal immune response to antigen-encoding DNA is
CC improves by complexing the DNA to lipospermine (esp. DOGS,
CC dioctadecylamidoglycylspermine) or lipospermidine which can
CC facilitate transfection. Antigens are pref. viral envelope proteins,
CC esp. HIV gp160 and its fragments. An immunisation construct DNAenv
CC was prepared which encoded the HIV-1 env protein. The construct was
CC transfected into mice either as naked DNA or as a complex with
CC DOGS. The persistence of DNAenv in tissues was determined by PCR
CC analysis using primers ED5 and ED12 (see AAT35933 and AAT35934) which
CC amplify a fragment of 1200 bp from the HIV V3-V5 region. The
CC presence of DOGS was shown to greatly improve transfection
CC efficiency.

XX Sequence 30 BP; 7 A; 11 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 26; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTTCTGCTGCTCCCAAGAACCC 26
|||||
Db 2 GTGCTTCTGCTGCTCCCAAGAACCC 27

RESULT 8

AAX25184/c

ID AAX25184 standard; DNA; 34 BP.

XX

AC AAX25184;

XX

DT 19-JUL-1999 (first entry)

DE HIV-1 group O gp41 region DNA primer 41-1.

XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
KW vaccine; diagnosis; AIDS; PCR; primer; ss.

XX Synthetic.

OS Human immunodeficiency virus type 1.

XX WO9904011-A2.

XX 28-JAN-1999.

XX 20-JUL-1998; 98WO-EP04522.

XX 18-JUL-1997; 97EP-0870110.

XX (INNO-) INNOGENETICS NV.

XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

XX WPI; 1999-132255/11.

XX New isolated HIV-1 group O strains - used to produce
PT polynucleotides, antigens and antibodies for use in diagnosis and in
PT vaccines for prevention of HIV-1 infection

XX Example 1; Page 61; 162pp; English.

XX This PCR primer, designated 41-1, is used as a sense primer in the
CC PCR amplification of part of the gp41 region of HIV-1 group O or
CC group M. Antisense primer 41-4 is given in AAX25185. Following the
CC amplification, nested PCR can be performed using primers 41-6 (see
CC AAX25186) and 41-7 (see AAX25187). The invention relates to new HIV-1
CC group O antigens (see AAY0546-625), including gp41 antigens, and the
CC use of these antigens, or nucleic acids encoding them (see
CC AAX25184-80), in the diagnosis and prophylaxis of AIDS. Vaccines that
CC provide protective immunity against HIV-1 group O infection comprise
CC at least one HIV-1 type O antigen, a nucleic acid encoding such an
CC antigen, a virus-like particle comprising such an antigen, or an
CC attenuated form of an HIV-1 type O strain. The invention also
CC relates to a method for genotyping HIV-1 or HIV-1 type O strains
CC involving amplifying HIV-1 nucleic acids using a suitable primer
CC pair.

XX Sequence 34 BP; 7 A; 6 C; 15 G; 6 T; 0 other;

Query Match 100.0%; Score 26; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTTCTGCTGCTCCCAAGAACCC 26
|||||

Db 26 GTGCTTCTGCTGCTCCCAAGAACCC 1

RESULT 9

AAD07432/c

ID AAD07432 standard; DNA; 24 BP.

XX

AC AAD07432;

XX 10-AUG-2001 (first entry)

XX HIV-1 env gene amplifying forward primer.

XX Genomic equivalent marker; cell quantification; real-time PCR;
KW nucleic acid quantification; molecular beacon; thymocyte proliferation;
KW T cell receptor; TCR; DNA deletion circle; thymic function; cancer;
KW chemotherapy; radiotherapy; immune system disorder; HIV-1; pathogen;
KW DiGeorge syndrome; congenital immunodeficiency disorder; virus;

KW dysproliferative disease; bone marrow transplant; infectious particle;
KW HIV-1; env gene; PCR primer; ss.
OS Human immunodeficiency virus type 1.
XX US6235504-B1.
XX 22-MAY-2001.
XX 11-JAN-2000; 2000US-0481288.
XX 11-JAN-1999; 98US-0115432.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang L, Lewin SR, Kostrikis L, Ho DD;
XX WPI; 2001-366408/38.
XX
XX Determining the number of copies per cell of a preselected
PT polynucleotide target sequence, for monitoring immune system recovery,
PT comprises quantifying at least one target sequence and at least one
PT genomic equivalent marker sequence -
XX Example 3; Column 29-30; 26pp; English.
XX
XX The invention relates to a method of determining in a nucleic acid sample
CC of cellular origin the number of copies per cell of a preselected
CC polynucleotide target sequence, comprising quantifying at least one
CC target sequence, one genomic equivalent marker sequence, and expressing
CC the number of copies of the target sequence per cell as a ratio between
CC the abundance of the target sequence and that of the genomic equivalent
CC marker. The quantification of target sequence and the genomic equivalent
CC marker sequence is performed using real-time PCR amplification using a
CC forward primer, a reverse primer and a molecular beacon capable of
CC binding to a subsequence within the target sequence and genomic
CC equivalent marker sequence. The genomic equivalent marker may be used
CC to identify other genetic sequences for use as genomic equivalent
CC markers. It is particularly useful in determining the number of copies of
CC a marker of thymocyte proliferation e.g. T cell receptor (TCR) gene DNA
CC deletion circles which are useful in assessing thymic function.
CC Measurement of thymic function is an indicator of the ability of immune
CC system to recover from or become reconstituted after therapies that
CC destroy immune cells, e.g. chemotherapy or radiotherapy. This is useful
CC in monitoring the course of diseases and therapies directed to diseases
CC involving immune system e.g. HIV-1 infection, congenital immunodeficiency
CC disorder e.g. DiGeorge syndrome, and iatrogenically-induced
CC immunodeficient states, e.g., by chemotherapy or radiotherapy for
CC treatment of dysproliferative diseases e.g. cancer, and in bone marrow
CC transplant. The method is also useful in determining number of genomes
CC and cells in a biological sample, monitoring thymic function with age, in
CC determining target sequences of a pathogen or infectious particles e.g.
CC viruses, bacteria, fungi and parasites on a per cell basis. Examples of
CC viral DNA sequences that can be quantified are HIV-1 proviral DNA (gag
CC and env regions) and human herpes virus 8 (HHV-8) ORF25.
CC The present sequence is a PCR primer used to amplify
CC Human immunodeficiency virus type 1 (HIV-1) env gene amplicon which
CC was used for assaying abundance of HIV-1 provirions on a per cell basis.
XX
SQ Sequence 24 BP; 6 A; 5 C; 8 G; 5 T; 0 other;
Query Match 88.5%; Score 23; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTTCCTGCTGCTCCCAAGAA 23
Db 23 GTGCTTCCTGCTGCTCCCAAGAA 1
RESULT 10
AAZ10963
ID AAZ10963 standard; DNA; 25 BP.

XX AAZ10963;
XX 29-OCT-1999 (first entry)
XX PCR primer for HIV-1 gp120 coding sequence.
XX Glycoprotein D; gp; recombinant antigen library; disease-related antigen;
KW multivalent antigenic polypeptide production; infection; allergen;
KW asthma; autoimmune disease; rheumatoid arthritis; diabetes; therapy;
KW multiple sclerosis; inflammatory condition; cancer; contraception;
KW immune response; PCR primer; ss.
XX Synthetic.
OS Human immunodeficiency virus type 1.
XX WO9941383-A1.
XX 19-AUG-1999.
XX 10-FEB-1999; 99WO-US02944.
XX 23-OCT-1998; 98US-0105509.
XX 11-FEB-1998; 98US-0021769.
XX 11-FEB-1998; 98US-0074294.
XX (MAXY-) MAXYGEN INC.
XX Bass SH, Howard R, Punnonen J, Stemmer WPC, Whalen RG;
XX WPI; 1999-518452/43.
XX Recombinant multivalent antigenic polypeptide produced by
PT recombining nucleic acid sequences and screening, used in vaccines
PT against e.g. infections and cancer
XX Example 8; Fig 8b; 153pp; English.
XX
XX This sequence represents a PCR primer for DNA encoding the HIV gp120
CC coding sequence. The amplified sequence was used to create a recombinant
CC antigen library. The library comprises recombinant nucleic acids encoding
CC antigenic polypeptides and is produced by recombination of at least two
CC forms of nucleic acid, differing by at least two nucleotides, encoding a
CC disease-related antigenic polypeptide. The library can be used to produce
CC a recombinant multivalent antigenic polypeptides of the invention, that
CC contains at least two antigenic determinants (AD) from different
CC polypeptides. The multivalent antigenic polypeptides are used in vaccines
CC to induce a protective or therapeutic response to a wide variety of
CC infectious agents (bacteria, viruses, parasites, including Plasmodium
CC falciparum); allergens; asthma; autoimmune disease (e.g. rheumatoid
CC arthritis, diabetes, multiple sclerosis); other inflammatory conditions
CC and cancer, also, where directed against sperm antigens, they can be used
CC for contraception. The multivalent peptides can be evolved to induce an
CC optimised immune response against a wide variety of antigens,
CC particularly a broad spectrum response to many different strains of a
CC pathogen, including strains that are likely to appear in the future.
XX
SQ Sequence 25 BP; 6 A; 11 C; 3 G; 5 T; 0 other;
Query Match 88.5%; Score 23; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CTTCTGCTGCTGCCCAAGAACCC 26
Db 1 CTTCTGCTGCTGCCCAAGAACCC 23
RESULT 11
AAQ40104
ID AAQ40104 standard; DNA; 28 BP.
XX
XX AAZ10963 standard; DNA; 25 BP.

XX The present invention relates to selenoproteins encoded in the genome of
CC a virus, where the coding sequence of the selenoprotein is genetically
CC engineered for expression in a nucleic acid construct. The invention also
CC discloses a method for identifying selenoprotein coding sequences, for
CC detecting certain viruses (e.g. HIV or Ebola), cancer and immune system
CC disorders. The present sequence was used to illustrate the invention.

XX SQ Sequence 38 BP; 6 A; 6 C; 14 G; 12 U; 0 other;

Query Match 80.8%; Score 21; DB 24; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCCTGCTGCTCCCAAGAACCC 26
|||||
Db 38 TCCTGCTGCTCCCAAGAACCC 18

RESULT 14

AAQ58958
ID AAQ58958 standard; DNA; 24 BP.

XX AC AAQ58958;

XX DT 04-NOV-1994 (first entry)

XX DE env d primer.

XX Human immunodeficiency virus; HIV; antigen; detection; diagnosis;
KW retrovirus; vaccine; lymphocyte; reverse transcriptase;
KW amplification; primer; polymerase chain reaction; PCR; ss.

XX OS Synthetic.

XX PN EP591914-A.

XX PD 13-APR-1994.

XX PF 05-OCT-1993; 93EP-0116058.

XX PR 06-OCT-1992; 92DE-4233646.

XX PR 22-OCT-1992; 92DE-4235718.

XX PR 30-DEC-1992; 92DE-4244541.

XX PR 01-JUN-1993; 93DE-4318186.

XX PA (BEHW) BEHRINGWERKE AG.

XX PI Brunn VA, Eberle J, Gurtler LG, Hauser H-P, Knapp S;

XX DR WPI; 1994-120077/15.

XX New HIV-type immune deficiency virus ECACC V 92092318 - and

XX deriv. cDNA or antigens, useful for diagnosing retroviral

XX infections and vaccines

XX Disclosure; Page 5; 73pp; German.

XX MVP-5180/91 DNA is obtained by PCR using the primers given

XX in AAQ58925-958.

SQ Sequence 24 BP; 6 A; 10 C; 5 G; 3 T; 0 other;

Query Match 76.9%; Score 20; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCTGCTGCTCCCAAGAACCC 26
|||||
Db 1 CCTGCTGCTCCCAAGAACCC 20

RESULT 15

AAAX22363
ID AAAX22363 standard; DNA; 24 BP.

XX AC AAAX22363;

XX DT 19-MAY-1999 (first entry)

XX DE HIV-2 PCR primer env d.

XX KW HIV-type retrovirus; MVP-5180/91; ECACC V 92092318; antigen; assay kit;
KW detection; antibody; immune deficiency; vaccine; PCR primer; ss.

XX OS Synthetic.

XX OS Human immunodeficiency virus type 2.

XX PN EP890642-A2.

XX PD 13-JAN-1999.

XX PF 05-OCT-1993; 93EP-0116058.

XX PR 01-JUN-1993; 93DE-4318186.

XX PR 06-OCT-1992; 92DE-4233646.

XX PR 22-OCT-1992; 92DE-4235718.

XX PR 30-DEC-1992; 92DE-4244541.

XX PA (DADE-) DADE BEHRING MARBURG GMBH.

XX PI Brunn AV, Eberle J, Guertler LG, Hauser H, Knapp S;

XX DR WPI; 1999-072878/07.

XX New HIV-type retrovirus and corresponding cDNA, recombinant DNA and

XX antigen - used for detecting retro-viruses that cause immune

XX deficiency and to prepare vaccines

XX Disclosure; Page 4; 39pp; German.

XX This invention describes the isolation of a novel HIV-type retrovirus
CC called MVP-5180/91 (ECACC V 92092318). Antigens produced from this
CC product can be used in an assay kit for detecting antibodies against
CC viruses that cause immune deficiency, preferably where the assay is a
CC Western blot, ELISA or fluorescence immunoassay. MVP-5180/91, cDNA
CC and/or antigen can be used for detecting retroviruses that cause immune
CC deficiency and to prepare vaccines. This sequence represents a PCR primer
CC used in the method of the invention.

XX SQ Sequence 24 BP; 6 A; 10 C; 5 G; 3 T; 0 other;

Query Match 76.9%; Score 20; DB 20; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCTGCTGCTCCCAAGAACCC 26
|||||

Db 1 CCTGCTGCTCCCAAGAACCC 20

Search completed: December 5, 2002, 23:00:21
Job time : 233.408 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 21:54:08 : Search time 1709.1 seconds
(without alignments)
442.731 Million cell updates/sec

Title: US-09-670-105-51
Perfect score: 26
Sequence: 1 GTGCTTCGTCTGCTGCCAGAACCC 26

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl :

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

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11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

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29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	26	100.0	26	6	A31980	A31980 Synthetic H
c	26	100.0	26	6	A31981	A31981 Synthetic H
3	26	100.0	26	6	AR131399	AR131399 Sequence
c	26	100.0	26	6	AR131400	AR131400 Sequence
4	26	100.0	26	6	BD001804	BD001804 Immunogen
c	26	100.0	26	6	BD001805	BD001805 Immunogen
7	26	100.0	27	6	AR066367	AR066367 Sequence
c	26	100.0	34	6	AX000842	AX000842 Sequence
9	23	88.5	24	6	AR153415	AR153415 Sequence
c	10	21	80.8	38	AR172210	AR172210 Sequence
11	20	76.9	24	6	A38027	A38027 Sequence 34
12	20	76.9	24	6	AR059451	AR059451 Sequence
13	20	76.9	24	6	AX001384	AX001384 Sequence
14	20	76.9	24	6	BD000313	BD000313 cDNA comp
15	19	73.1	36	6	AR017599	AR017599 Sequence
16	19	73.1	36	6	AR068245	AR068245 Sequence
17	18	69.2	18	6	AR017596	AR017596 Sequence
18	18	69.2	18	6	AR068242	AR068242 Sequence
19	18	69.2	40	6	A38020	A38020 Sequence 27
c	20	18	69.2	40	AR017597	AR017597 Sequence
21	18	69.2	40	6	AR059444	AR059444 Sequence
c	22	18	69.2	40	AR068243	AR068243 Sequence
23	18	69.2	40	6	AX001377	AX001377 Sequence
24	18	69.2	40	6	BD000306	BD000306 cDNA comp
c	25	17	65.4	21	AX472697	AX472697 Sequence
c	26	17	65.4	39	A24307	A24307 North Ameri
c	27	15	57.7	20	A24306	A24306 SK68 consen
c	28	15	57.7	20	A24322	A24322 SK68 primer
c	29	15	57.7	20	A38014	A38014 Sequence 21
c	30	15	57.7	20	A38028	A38028 Sequence 35
c	31	15	57.7	20	AR059438	AR059438 Sequence
c	32	15	57.7	20	AR059452	AR059452 Sequence
c	33	15	57.7	20	AX001371	AX001371 Sequence
c	34	15	57.7	20	AX001385	AX001385 Sequence
c	35	15	57.7	20	BD000300	BD000300 cDNA comp
c	36	15	57.7	20	BD000314	BD000314 cDNA comp
c	37	15	57.7	20	E11671	E11671 PCR primer
c	38	14	53.8	20	AR032116	AR032116 Sequence
39	14	53.8	20	6	AX472702	AX472702 Sequence
40	14	53.8	50	6	AX133389	AX133389 Sequence
41	13	50.0	21	6	AX428503	AX428503 Sequence
42	13	50.0	30	6	AX428442	AX428442 Sequence
43	13	50.0	30	6	AX428474	AX428474 Sequence
44	12	46.2	20	6	AR032115	AR032115 Sequence
45	12	46.2	20	6	AR200892	AR200892 Sequence

ALIGNMENTS

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LOCUS	Synthetic HIV-1/2 diagnosis primer.					
DEFINITION	A31980					
ACCESSION	A31980					
VERSION	A31980.1	GI:1567263				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						

synthetic construct.
synthetic construct.
artificial sequences.
1 (bases 1 to 26)
Moncany, M. and Montagnier, L.
Nucleotide sequences of retroviral genomes of types HIV-1, HIV-2
and SIV, their uses for the amplification of these genomes and
diagnosis in vitro of these viral infections

JOURNAL Patent: EP 0403333-A 35 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
MEDICALE (INSERM)
FEATURES Location/Qualifiers
source
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/db_xref="taxon:32630"

BASE COUNT 4 a 11 c 5 g 6 t
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTTCCTGCTGCTCCCAAGAACC 26
Db 1 GTGCTTCCTGCTGCTCCCAAGAACC 26

RESULT 2

A31981/c A31981 26 bp DNA linear PAT 08-JUL-1996
LOCUS Synthetic HIV-1/2 diagnosis primer.
DEFINITION A31981
ACCESSION A31981
VERSION A31981.1 GI:1567264

KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 26)

AUTHORS Moncany,M. and Montagnier,L.

TITLE Nucleotide sequences of retroviral genomes of types HIV-1, HIV-2 and HIV, their uses for the amplification of these genomes and diagnosis in vitro of these viral infections

PATENT: EP 0403333-A 36 19-DEC-1990;

JOURNAL INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE

MEDICALE (INSERM)

FEATURES Location/Qualifiers

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/organism="synthetic construct"

/db_xref="taxon:32630"

BASE COUNT 6 a 5 c 11 g 4 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTTCCTGCTGCTCCCAAGAACC 26
Db 26 GTGCTTCCTGCTGCTCCCAAGAACC 1

RESULT 3

A313399 A313399 26 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 51 from patent US 6194142.
DEFINITION A313399
ACCESSION A313399
VERSION A313399.1 GI:14120302

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 26)

AUTHORS Moncany,M. and Montagnier,L.

TITLE Nucleotide sequences derived from the genome of retroviruses of the HIV-1, HIV-2, and HIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the in vitro diagnosis of the diseases due to these viruses

PATENT: US 6194142-A 51 27-FEB-2001;

JOURNAL

FEATURES Location/Qualifiers

source 1..26

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RESULT 4

ARI31400/c ARI31400 26 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 52 from patent US 6194142.
DEFINITION ARI31400
ACCESSION ARI31400
VERSION ARI31400.1 GI:14120303

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 26)

AUTHORS Moncany,M. and Montagnier,L.

TITLE Nucleotide sequences derived from the genome of retroviruses of the HIV-1, HIV-2, and HIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the in vitro diagnosis of the diseases due to these viruses

PATENT: US 6194142-A 52 27-FEB-2001;

JOURNAL

FEATURES Location/Qualifiers

source 1..26

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BASE COUNT 6 a 5 c 11 g 4 t

ORIGIN

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTTCCTGCTGCTCCCAAGAACC 26
Db 26 GTGCTTCCTGCTGCTCCCAAGAACC 1

RESULT 5

BD001804 BD001804 26 bp DNA linear PAT 31-JAN-2002
LOCUS Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and HIV types.
DEFINITION BD001804
ACCESSION BD001804.1 GI:18626363
VERSION JP 2000093187-A/51
KEYWORDS synthetic construct.
SOURCE artificial construct.
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 26)

AUTHORS Moncany,M. and Montagnier,L.

TITLE Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and HIV types

PATENT: JP 2000093187-A 51 04-APR-2000;

JOURNAL INST PASTEUR, INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL

COMMENT OS Artificial Sequence

PN JP 2000093187-A/51

PD 04-APR-2000

PF 24-SEP-1999 JP 1999270165

PI 02-JUN-1989 FR 89/07354, 20-SEP-1989 FR 89/12371

PC MAURICE MONCANY, LUC MONTAGNIER

PC C12N15/09, A61K39/21, A61K48/00, A61P31/18, C07H21/04, C07K14/155,

PC C07K14/16,

PC C12Q1/68, C12Q1/70, G01N33/569, C12N15/00

CC

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Db 1 GTGCTTCTGCTGCTCCCAAGAACC 26
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RESULT 6

BD001805/c

LOCUS BD001805 26 bp DNA linear PAT 31-JAN-2002
DEFINITION Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
types.

ACCESSION BD001805

VERSION BD001805.1 GI:18626364

KEYWORDS JP 2000093187-A/52.

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 26)

AUTHORS Moncany, M. and Montagnier, L.

TITLE Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
types

JCURNAL

COMMENT INST PASTEUR, INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL

OS Artificial Sequence

PN JP 2000093187-A/52

PD 04-APR-2000

PF 24-SEP-1999 JP 1999270165

PR 02-JUN-1989 FR 89/07354, 20-SEP-1989 FR 89/12371 PI

MAURICE MONCANY, LUC MONTAGNIER

PC C12N15/09, A61K39/21, A61K48/00, A61P31/18, C07H21/04, C07K14/155,

PC C07K14/16,

PC C12Q1/68, C12Q1/70, G01N33/569, C12N15/00

CC FH Key Location/Qualifiers

FT source 1..26

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source Location/Qualifiers
/organism='Artificial Sequence'.
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ORIGIN
/organism='synthetic construct'
/db_xref='taxon:32630'

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Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTTCTGCTGCTCCCAAGAACC 26
|||||

Db 26 GTGCTTCTGCTGCTCCCAAGAACC 1
|||||

RESULT 7

AR066367

LOCUS AR066367 27 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 6 from patent US 5849994.

ACCESSION AR066367

VERSION AR066367.1 GI:5996583

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Narayan, O.
TITLE Animal model for HIV-1 induced disease
JOURNAL Patent: US 5849994-A 6 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..27
/organism='unknown'
BASE COUNT 5 a 11 c 5 g 6 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTTCTGCTGCTCCCAAGAACC 26
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Db 2 GTGCTTCTGCTGCTCCCAAGAACC 27
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RESULT 8

AX000842/c

LOCUS AX000842 34 bp DNA linear PAT 10-MAR-2000

DEFINITION Sequence 139 from Patent WO9904011.

ACCESSION AX000842

VERSION AX000842.1 GI:7241107

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 34)

AUTHORS Vanden, H.M. and Saman, E.

TITLE HIV-1 GROUP O ANTIGENS AND USES THEREOF

JOURNAL Patent: WO 9904011-A 139 28-JAN-1999;

VANDEN HAESEVELDE MARLEEN (BE); INNOGENETICS NV (BE)

FEATURES

source 1..34

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/db_xref='taxon:32644'

BASE COUNT 7 a 6 c 15 g 6 t

ORIGIN

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 26 GTGCTTCTGCTGCTCCCAAGAACC 1
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RESULT 9

AR153415/c

LOCUS AR153415 24 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 23 from patent US 6235504.

ACCESSION AR153415

VERSION AR153415.1 GI:15120947

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Zhang, L., Lewin, S.R., Kostrikis, L. and Ho, D.D.

TITLE Methods for identifying genomic equivalent markers and their use in
quantitating cells and polynucleotide sequences therein

JOURNAL Patent: US 6235504-A 23 22-MAY-2001;

FEATURES

source 1..24

/organism='unknown'

BASE COUNT 6 a 5 c 8 g 5 t

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Query Match 88.5%; Score 23; DB 6; Length 24;
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QY 1 GTGCTTCCTGCTGCCCAAGAA 23

Db 23 GTGCTTCCTGCTGCCCAAGAA 1

RESULT 10

LOCUS ARI72210/c ARI72210 38 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 32 from patent US 6303295.

ACCESSION ARI72210

VERSION ARI72210.1 GI:17911701

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 38)

AUTHORS Taylor,E.Will., Nadimpalli,R.Gopal. and Ramanathan,C.Sekar.

TITLE Selenoproteins, coding sequences and methods

JOURNAL Patent: US 6303295-A 32 16-OCT-2001;

FEATURES Location/Qualifiers

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Source /organism="unknown"

BASE COUNT 6 a 6 c 14 g 12 t

ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db :38 TCCTGCTGCTCCCAAGAACCC 18

RESULT 11

LOCUS A38027 A38027 24 bp DNA linear PAT 05-MAR-1997

DEFINITION Sequence 34 from Patent EP0591914.

ACCESSION A38027

VERSION A38027.1 GI:2294683

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Guertler,L.G., Eberle,J.D., Brunn,V.A., Dr, Knapp,S.D. and

Hauser,H.D.

TITLE Retrovirus of the HIV-group and its application

JOURNAL Patent: EP 0591914-A 34 13-APR-1994;

COMMENT BEHRINGWERKE AG (DE)

Other publication AU 4880093 940421

Other publication CA 2107732 940407

Other publication JP 6225760 940816

Other publication ZA 9307371 940429

Other publication DE 4235718 940428

Other publication DE 4244541 940707

Other publication DE 4233646 940407.

FEATURES

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Db 1 CCTGCTGCTCCCAAGAACCC 20

RESULT 12

LOCUS AR059451 AR059451

DEFINITION Sequence 34 from patent US 5840480.

ACCESSION AR059451

VERSION AR059451.1 GI:5985901

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Guertler,L.G., Eberle,J., Brunn,Av., Knapp,S. and Hauser,H.-P.

TITLE Retrovirus from the HIV group and its use

JOURNAL Patent: US 5840480-A 34 24-NOV-1998;

FEATURES Location/Qualifiers

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Source /organism="unknown"

BASE COUNT 6 a 10 c 5 g 3 t

ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTGCTGCTCCCAAGAACCC 26

Db 1 CCTGCTGCTCCCAAGAACCC 20

RESULT 13

LOCUS AX001384 AX001384

DEFINITION Sequence 34 from Patent EP0890642.

ACCESSION AX001384

VERSION AX001384.1 GI:7241558

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Guertler,L.G. and V.B.A.

TITLE Retrovirus of the HIV-group and its application

JOURNAL Patent: EP 0890642-A 34 13-JAN-1999;

FEATURES Location/Qualifiers

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Source /organism="unidentified"

BASE COUNT 6 a 10 c 5 g 3 t

ORIGIN

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Db 1 CCTGCTGCTCCCAAGAACCC 20

RESULT 14

LOCUS BD000313 BD000313

DEFINITION CDNA complementary to RNA of immunodeficiency virus of hiv group.

ACCESSION BD000313

VERSION BD000313.1 GI:18623392

KEYWORDS

JP 2000312592-A/34.

SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gurutora,L.G., Evelre,J., Brunne,A.F., Knapp,S. and Hauser,H.P.
TITLE CDNA complementary to RNA of immunodeficiency virus of hiv group
JOURNAL Patent: JP 2000312592-A 34 14-NOV-2000;
COMMENT DEIDO BEORRING MARUBURUKU GMBH
OS Artificial Sequence
PN JP 2000312592-A/34
PD 14-NOV-2000
PF 23-FEB-2000 JP 2000045662
PR 06-OCT-1992 DE P4233646:5,22-OCT-1992 DE P4235718:7 PR
30-DEC-1992 DE P4244541:8,01-JUN-1993 DE P4318186:4 PI LUTZ G
GURUTORA,JOSEPH EVELRE,ALBRECHT FAU BRUNNE, PI STEPHEN KNAPP,
PI HANS PATER HAUSER
PC C12N15/09,C07K14/155,C12N7/00,C12Q1/68,G01N33/569//A61K39/21,
PC A61P31/18,
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Db 1 CCTGCTGCTCCCAAGACCC 20

RESULT 15
AR017599
LOCUS AR017599 36 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 5 from patent US 5780227.
ACCESSION AR017599
VERSION AR017599.1 GI:3973202
KEYWORDS
SOURCE unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 36)
AUTHORS Sheridan,P.J., Gagne,J.C. and Anderson,M.L.
TITLE Oligonucleotide probe conjugated to a purified hydrophilic alkaline
phosphatase and uses thereof
JOURNAL Patent: US 5780227-A 5 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..36
/organism='unknown'

BASE COUNT 6 a 9 c 9 g 12 t
ORIGIN

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Qy 5 TTCCTGCTGCTCCCAAGAA 23
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Db 18 TTCCTGCTGCTCCCAAGAA 36

Search completed: December 5, 2002, 23:54:17
Job time : 1710.1 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 22:51:23 ; Search time 1425.53 Seconds
(without alignments)
261.304 Million cell updates/sec

Title: US-09-670-105-48

Perfect score: 23

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Scoring table: OLIGO_NUC

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Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	11	47.8	48	BH864584	BH864584 SALK_0962
5	11	47.8	50	AU106268	AU106268
6	10	43.5	19	AZ795136	AZ795136 2M0049A16

c	7	10	43.5	23	17	AZ309461
c	8	10	43.5	27	17	AZ843637
c	9	10	43.5	28	9	AA873218
c	10	10	43.5	28	9	A1810043
c	11	10	43.5	30	17	AZ804486
c	12	10	43.5	31	9	A1338567
c	13	10	43.5	34	17	AZ773199
c	14	10	43.5	34	17	AZ805966
c	15	10	43.5	37	9	A1479308
c	16	10	43.5	38	17	AZ816996
c	17	10	43.5	39	17	AZ592385
c	18	10	43.5	40	9	AA990516
c	19	10	43.5	40	9	AA238160
c	20	10	43.5	43	9	AA390187
c	21	10	43.5	44	9	AA231947
c	22	10	43.5	45	17	AZ511021
c	23	10	43.5	47	17	AZ606685
c	24	10	43.5	48	17	AZ629734
c	25	10	43.5	49	9	AA500776
c	26	10	43.5	49	14	W71090
c	27	10	43.5	49	17	AZ658888
c	28	10	43.5	50	9	AU103811
c	29	10	43.5	50	9	AU104063
c	30	10	43.5	50	9	AU104064
c	31	10	43.5	50	9	AU104065
c	32	10	43.5	50	9	AU104066
c	33	10	43.5	50	17	AZ608907
c	34	10	43.5	50	17	AZ658253
c	35	9	39.1	19	17	AZ643528
c	36	9	39.1	20	9	AU256704
c	37	9	39.1	20	17	AZ582434
c	38	9	39.1	20	17	AZ786334
c	39	9	39.1	22	17	AZ855118
c	40	9	39.1	22	17	BH000100
c	41	9	39.1	22	17	PCB304096
c	42	9	39.1	23	17	AZ389539
c	43	9	39.1	23	17	AZ793609
c	44	9	39.1	24	17	AZ366164
c	45	9	39.1	24	17	BH864943

ALIGNMENTS

RESULT 1
AU104331
LOCUS AU104331 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION COLF0073, mRNA sequence.
ACCESSION AU104331
VERSION AU104331.1 GI:13553852
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
TITLE EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE Contact: Yutaka Suzuki
COMMENT Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
Location/Qualifiers

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source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF0073"
/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"
17 a 9 c 17 g 7 t

BASE COUNT
ORIGIN

Query Match 52.2%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.1e-04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AGCAGAAGAAGA 23
|||||
DB 35 AGCAGAAGAAGA 46

RESULT 2
AZ762628/c
LOCUS
DEFINITION
1M0557A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0557A16 R, DNA sequence.
ACCESSION
AZ762628
VERSION
AZ762628.1 GI:12872834
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0557 row: A column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
FEATURES
source
1. 37
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0557A16"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42hv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

```

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
7 a 10 c 10 g 10 t

BASE COUNT
ORIGIN

Query Match 47.8%; Score 11; DB 17; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.5e-04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCAGAAGAAGA 23
|||||
DB 22 GCAGAAGAAGA 12

RESULT 3
TA89E09P
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 89e09, forward sequence,
genomic survey sequence.
ACCESSION
AL461090
VERSION
AL461090.1 GI:11862342
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 40)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
Location/Qualifiers
1. 40
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="89e09"

BASE COUNT
ORIGIN
20 a 5 c 10 g 5 t

Query Match 47.8%; Score 11; DB 17; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.6e-04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCAGAAGAAGA 23
|||||
DB 24 GCAGAAGAAGA 34

RESULT 4
BH864584/c
LOCUS
BH864584
48 bp DNA linear GSS 05-AUG-2002

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DEFINITION SALK_096296 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_096296, DNA sequence.

ACCESSION BH864584

VERSION BH864584.1 GI:22100482

KEYWORDS GSS.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.

AUTHORS A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

TITLE Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .48
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_096296"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 10 a 19 c 2 g 17 t

ORIGIN

Query Match 47.8%; Score 11; DB 17; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AGCAGAAGAAG 22
|||||
Db 45 AGCAGAAGAAG 35

RESULT 5

AU106268

LOCUS AU106268 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

DEFINITION CASI1437, mRNA sequence.

ACCESSION AU106268

VERSION AU106268.1 GI:13555789

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yasukie@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CASI1437"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT 12 a 11 c 19 g 8 t

ORIGIN

Query Match 47.8%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AGTCTAGCAGA 17
|||||
Db 7 AGTCTAGCAGA 17

RESULT 6

AZ795136

LOCUS AZ795136 19 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0049A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0049A16 F, DNA sequence.

ACCESSION AZ795136

VERSION AZ795136.1 GI:12941845

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0049 row: A column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0049A16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

DEFINITION SALK_096296 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_096296, DNA sequence.

ACCESSION BH864584

VERSION BH864584.1 GI:22100482

KEYWORDS GSS.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.

AUTHORS A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

TITLE Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .48
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_096296"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 10 a 19 c 2 g 17 t

ORIGIN

Query Match 47.8%; Score 11; DB 17; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AGCAGAAGAAG 22
|||||
Db 45 AGCAGAAGAAG 35

RESULT 5

AU106268

LOCUS AU106268 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

DEFINITION CASI1437, mRNA sequence.

ACCESSION AU106268

VERSION AU106268.1 GI:13555789

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yasukie@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CASI1437"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT 12 a 11 c 19 g 8 t

ORIGIN

Query Match 47.8%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AGTCTAGCAGA 17
|||||
Db 7 AGTCTAGCAGA 17

RESULT 6

AZ795136

LOCUS AZ795136 19 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0049A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0049A16 F, DNA sequence.

ACCESSION AZ795136

VERSION AZ795136.1 GI:12941845

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0049 row: A column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0049A16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 3 c 5 g 4 t
ORIGIN

Query Match 43.5%; Score 10; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TAGCAGAAGA 20
|||||

Db 10 TAGCAGAAGA 19

RESULT 7
AZ309461/c
LOCUS
DEFINITION 23 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0013G17 R, DNA sequence.

ACCESSION AZ309461
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0013 row: G column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source
1..23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0013G17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 4 c 6 g 13 t
ORIGIN

Query Match 43.5%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CAGAGAAGA 23
|||||

Db 20 CAGAGAAGA 11

RESULT 8
AZ843637/c
LOCUS
DEFINITION 27 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0142006 R, DNA sequence.

ACCESSION AZ843637
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: 0 column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source
1..27
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0142006"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 8 t

BASE COUNT 2 a 5 c 12 g

ORIGIN

Query Match 43.5%; Score 10; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TAGCAGAACA 20
|||||

DB 10 TAGCAGAACA 1

RESULT 9
LOCUS AA873218 28 bp mRNA linear EST 29-APR-1998
DEFINITION oh70f08.s1 NCI-CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472391 3' similar to SW:NUPM_BOVIN P42029 NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT ;, mRNA sequence.

ACCESSION AA873218
VERSION AA873218.1 GI:2969340
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Cloning Strategy: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1784 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1472391"
/clone_lib="NCI-CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACGTGAGATTCGCGCGCAATATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors

BASE COUNT 2 a 5 c 12 g

ORIGIN

Query Match 43.5%; Score 10; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ACCACAAGAA 21
|||||

DB 21 AGCAGAAGAA 12

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 9 a 6 c 5 g 8 t

ORIGIN

Query Match 43.5%; Score 10; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGCCAGTC 10
|||||

DB 11 AATGCCAGTC 20

RESULT 10
LOCUS AI810043/c 28 bp mRNA linear EST 19-DEC-1999
DEFINITION wf79f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361827 3' similar to TR:O60281 KIAA0530 PROTEIN ;, mRNA sequence.

ACCESSION AI810043
VERSION AI810043.1 GI:5396609
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 746 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2361827"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 3 a 7 c 5 g 13 t

ORIGIN

Query Match 43.5%; Score 10; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ACCACAAGAA 21
|||||

DB 21 AGCAGAAGAA 12

RESULT 11

AZ804486
LOCUS 30 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0065D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0065D07 F, DNA sequence.

ACCESSION AZ804486
VERSION AZ804486.1 GI:12956809
KEYWORDS GSS.
SOURCE house mouse,
Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddund@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0065 row: D column: 07

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 30.

FEATURES

source

1..30

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0065D07"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 9 a 1 c 18 g 2 t
ORIGIN

Query Match 43.5%; Score 10; DB 17; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

14 CAGAGAAGA 23

|||||

Db

5 CAGAGAAGA 14

RESULT 12

A1338567/c

LOCUS

DEFINITION

q998f04.x1 Soares_total_fetus.Nb2HF8_9w Homo sapiens CDNA clone

IMAGE:1939423 3' similar to TR:Q66660 Q66660 ORF 59. ; mRNA

sequence.

ACCESSION A1338567

VERSION A1338567

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1382 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1..31

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1939423"

/clone_lib="Soares_total_fetus.Nb2HF8_9w"

/dev_stage="8-9 weeks"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from pooled 8-9 week

(total) fetus material with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 8 c 4 g 17 t

ORIGIN

Query Match 43.5%; Score 10; DB 9; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CAGAGAAGA 23

|||||

Db 15 CAGAGAAGA 6

RESULT 13

AZ773199

LOCUS

DEFINITION

1M0584P04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0584P04 R, DNA sequence.

ACCESSION AZ773199

VERSION AZ773199.1 GI:12897312

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 34)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

A1338567 31 bp mRNA linear EST 13-FEB-1999
q998f04.x1 Soares_total_fetus.Nb2HF8_9w Homo sapiens CDNA clone
IMAGE:1939423 3' similar to TR:Q66660 Q66660 ORF 59. ; mRNA
sequence.

ACCESSION A1338567

VERSION A1338567

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1382 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1..31

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1939423"

/clone_lib="Soares_total_fetus.Nb2HF8_9w"

/dev_stage="8-9 weeks"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from pooled 8-9 week

(total) fetus material with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 8 c 4 g 17 t

ORIGIN

Query Match 43.5%; Score 10; DB 9; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CAGAGAAGA 23

|||||

Db 15 CAGAGAAGA 6

RESULT 13

AZ773199

LOCUS

DEFINITION

1M0584P04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0584P04 R, DNA sequence.

ACCESSION AZ773199

VERSION AZ773199.1 GI:12897312

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 34)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

A1338567 31 bp mRNA linear EST 13-FEB-1999
q998f04.x1 Soares_total_fetus.Nb2HF8_9w Homo sapiens CDNA clone
IMAGE:1939423 3' similar to TR:Q66660 Q66660 ORF 59. ; mRNA
sequence.

ACCESSION A1338567

VERSION A1338567

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1382 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1..31

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1939423"

/clone_lib="Soares_total_fetus.Nb2HF8_9w"

/dev_stage="8-9 weeks"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from pooled 8-9 week

(total) fetus material with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0584 row: P column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.

FEATURES Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0584P04"
/clone_lib="Mouse 10Kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 5 c 5 g 12 t

ORIGIN

Query Match 43.5%; Score 10; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTAGCAGAAG 19
|||||
Db 9 CTAGCAGAAG 18

RESULT 14

LOCUS A2805966 34 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0067L07R Mouse 10Kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0067L07 R, DNA sequence.

ACCESSION A2805966

VERSION A2805966.1 GI:12966777

KEYWORDS GSS.

SOURCE house mouse.
Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 34)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: L column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.

FEATURES Location/Qualifiers
1..34
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0067L07"
/clone_lib="Mouse 10Kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 5 c 9 g 8 t

ORIGIN

Query Match 43.5%; Score 10; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTAGCAGAAG 19
|||||
Db 10 CTAGCAGAAG 19

RESULT 15

LOCUS A1479308 37 bp mRNA linear EST 14-APR-1999

DEFINITION tm27a05.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:215776 3' similar to SW:Y273_HUMAN Q92561 HYPOTHETICAL PROTEIN KIAA0273. ;, mRNA sequence.

ACCESSION A1479308

VERSION A1479308.1 GI:4372476

KEYWORDS EST.

SOURCE human.
Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 37)

REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-f@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1042 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES

source

1. .37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2157776"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI-CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 9 a 11 c 4 g 13 t
ORIGIN

Query Match 43.5%; Score 10; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 CAGAGAAGA 23
| | | | | | | |
Db -21 CAGAGAAGA 12

Search completed: December 6, 2002, 00:45:08
Job time : 1428.53 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 20:34:23 ; Search time 43.1837 Seconds
(without alignments)
163.339 Million cell updates/sec

Title: US-09-670-105-48

Perfect score: 23

Sequence: 1 AATGGCAGTCTAGCAGAAGAAGA 23

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	23	4	US-09-092-077-48
2	23	100.0	42	2	US-08-850-049-95
3	23	100.0	42	2	US-08-050-478-95
4	23	100.0	42	4	US-09-414-117-95
5	23	100.0	42	4	US-09-678-437-95
6	20	87.0	20	1	US-08-271-880A-183
7	20	87.0	20	2	US-08-910-408-183
8	20	87.0	20	3	US-09-249-215-183
9	20	87.0	20	4	US-08-722-015A-19
10	19	82.6	31	1	US-08-470-202-25
11	19	82.6	31	1	US-08-471-770-25
12	19	82.6	31	2	US-08-468-059-25
13	19	82.6	31	4	US-09-109-916-25
14	17	73.9	30	1	US-08-050-441-1
15	17	73.9	30	1	US-08-050-441-3
16	17	73.9	30	1	US-08-102-474-3
17	17	73.9	30	1	US-08-051-446-2
18	17	73.9	30	1	US-08-051-446-4
19	17	73.9	30	1	US-08-414-019A-3
20	17	73.9	30	5	PCT-US91-08523-1
21	17	73.9	30	5	PCT-US91-08523-3
22	15	65.2	33	3	US-07-850-770-29
23	15	65.2	33	5	PCT-US93-01598-29
24	13	56.5	25	2	US-08-488-199-1
25	13	56.5	46	1	US-08-006-845-22
26	12	52.2	24	4	US-09-324-867-52
27	12	52.2	37	3	US-09-091-058-18

c	28	12	52.2	42	3	US-09-109-063-36	Sequence 36, Appl
	29	12	52.2	44	3	US-09-109-063-37	Sequence 37, Appl
c	30	12	52.2	44	3	US-09-091-058-19	Sequence 19, Appl
	31	11	47.8	14	1	US-08-242-664-24	Sequence 24, Appl
	32	11	47.8	14	1	US-08-484-138-24	Sequence 24, Appl
	33	11	47.8	14	5	PCT-US95-06379-24	Sequence 24, Appl
c	34	11	47.8	16	1	US-08-283-591-21	Sequence 21, Appl
c	35	11	47.8	16	1	US-08-088-658-39	Sequence 39, Appl
c	36	11	47.8	16	2	US-08-471-907A-39	Sequence 39, Appl
c	37	11	47.8	16	4	US-08-088-661F-34	Sequence 34, Appl
c	38	11	47.8	16	4	US-08-150-156A-32	Sequence 32, Appl
c	39	11	47.8	16	4	US-08-108-591B-34	Sequence 34, Appl
c	40	11	47.8	17	1	US-08-373-124A-592	Sequence 592, App
c	41	11	47.8	17	1	US-08-373-124A-594	Sequence 594, App
c	42	11	47.8	17	1	US-08-373-124A-596	Sequence 596, App
c	43	11	47.8	17	1	US-08-373-124A-598	Sequence 598, App
c	44	11	47.8	17	1	US-08-373-124A-1631	Sequence 1631, Ap
c	45	11	47.8	17	1	US-08-373-124A-1633	Sequence 1633, Ap

ALIGNMENTS

RESULT 1

US-09-092-077-48
; Sequence 48, Application US/09092077
; Patent No. 6194142
; GENERAL INFORMATION:
; APPLICANT: Moncany, Maurice
; APPLICANT: Montagnier, Luc
; TITLE OF INVENTION: Nucleotide Sequences Derived From The
; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type.
; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis
; TITLE OF INVENTION: Of The Diseases Due To Those Viruses
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,077
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,928
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/160,465
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 8912371
; FILING DATE: 20-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 8907354
; FILING DATE: 06-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0062-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEPHONE: (202)408-4400
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-092-077-48

Query Match 100.0%; Score 23; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCAGTCTAGCAGAAGA 23
Db 1 AATGGCAGTCTAGCAGAAGA 23

RESULT 2

US-08-850-049-95
; Sequence 95, Application US/08850049
; Patent No. 5965726
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:

; TITLE OF INVENTION: METHOD OF ELIMINATING
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,049
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,478
; FILING DATE: 26-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02908
; FILING DATE: 29-MAR-1993

; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2026-40060US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)751-6849
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
US-08-850-049-95

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCAGTCTAGCAGAAGA 23
Db 13 AATGGCAGTCTAGCAGAAGA 35

RESULT 3

US-08-050-478-95
; Sequence 95, Application US/08050478
; Patent No. 5972596
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:

; TITLE OF INVENTION: METHOD OF ELIMINATING
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,478
; FILING DATE: 26-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02908
; FILING DATE: 29-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,747
; FILING DATE: 27-MAR-1992

; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2026-40060US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)751-6849
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
US-08-050-478-95

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCAGTCTAGCAGAAGA 23
Db 13 AATGGCAGTCTAGCAGAAGA 35

RESULT 4

US-09-414-117-95
; Sequence 95, Application US/09414117
; Patent No. 6291664
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:

;; TITLE OF INVENTION: METHOD OF ELIMINATING
;; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
;; NUMBER OF SEQUENCES: 130
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/414,117
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/850,049
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/02908
;; FILING DATE: 29-MAR-1993
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/858,747
;; FILING DATE: 27-MAR-1992
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MORRY, MARY J.
;; REGISTRATION NUMBER: 34,398
;; REFERENCE/DOCKET NUMBER: 2026-4006US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)758-4800
;; TELEFAX: (212)751-6849
;; INFORMATION FOR SEQ ID NO: 95:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 BASE PAIRS
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: LINEAR
;; US-09-414-117-95
Query Match 100.0%; Score 23; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGGCAGTCTAGCAGAAGA 23
Db 13 AATGGCAGTCTAGCAGAAGA 35
RESULT 5
US-09-678-437-95
; Sequence 95, Application US/09678437
; Patent No. 6414132
; GENERAL INFORMATION:
; APPLICANT: <Unknown>
; TITLE OF INVENTION: METHOD OF ELIMINATING
; INHIBITORY/INSTABILITY REGIONS OF mRNA
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK

;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/678,437
;; FILING DATE: 02-Oct-2000
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/850,049
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: PCT/US93/02908
;; FILING DATE: 29-MAR-1993
;; APPLICATION NUMBER: US 07/858,747
;; FILING DATE: 27-MAR-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MORRY, MARY J.
;; REGISTRATION NUMBER: 34,398
;; REFERENCE/DOCKET NUMBER: 2026-4006US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)758-4800
;; TELEFAX: (212)751-6849
;; INFORMATION FOR SEQ ID NO: 95:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 BASE PAIRS
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: LINEAR
;; US-09-678-437-95
Query Match 100.0%; Score 23; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGGCAGTCTAGCAGAAGA 23
Db 13 AATGGCAGTCTAGCAGAAGA 35
RESULT 6
US-08-271-880A-183
; Sequence 183, Application US/08271880A
; Patent No. 5693535
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,880A
; FILING DATE: July 7, 1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: two

; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-880A-183

Query Match 87.0%; Score 20; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 0.031;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCAGTCTAGCAGAAG 22
:||||:|||||
Db 1 UGGCAGUCUAGCAGAAG 20

RESULT 7

US-08-910-408-183
; Sequence 183, Application US/08910408
; Patent No. 5972704
; GENERAL INFORMATION:

; APPLICANT: Kenneth G. Draper

; APPLICANT: Bharat Chowrira

; APPLICANT: James McSwiggen

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James D. Thompson

; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING

; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 232

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/910,408

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/271,880

; FILING DATE: July 7, 1994

; APPLICATION NUMBER: 08/103,243

; FILING DATE: August 6, 1993

; APPLICATION NUMBER: 07/882,886

; FILING DATE: May 14, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 206/116

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-910-408-183

Query Match 87.0%; Score 20; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 0.031;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCAGTCTAGCAGAAG 22
:||||:|||||
Db 1 UGGCAGUCUAGCAGAAG 20

RESULT 8

US-09-249-215-183

; Sequence 183, Application US/09249215

; Patent No. 6159692

; GENERAL INFORMATION:

; APPLICANT: Kenneth G. Draper

; APPLICANT: Bharat Chowrira

; APPLICANT: James McSwiggen

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James D. Thompson

; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING

; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 232

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/249,215

; FILING DATE: 12-Feb-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/910,408

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/103,243

; FILING DATE: August 6, 1993

; APPLICATION NUMBER: 07/882,886

; FILING DATE: May 14, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 206/116

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 183:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 183:

US-09-249-215-183

Query Match 87.0%; Score 20; DB 3; Length 20;
Best Local Similarity 85.0%; Pred. No. 0.031;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCAGTCTAGCAGAAGAAG 22
:||||:|||||
Db 1 UGGCAGUCUAGCAGAAGAAG 20

RESULT 9

US-08-722-015A-19
; Sequence 19, Application US/08722015A
; Patent No. 6379881
; GENERAL INFORMATION:
; APPLICANT: Fouchier, Ronaldus A.M.
; APPLICANT: Schuitemaker, Johanna
; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTII
; TITLE OF INVENTION: INDUCING AND NON SYNCYTII INDUCING VARIANTS OF THE HUMAN IMMUN
; FILE REFERENCE: 9250.25
; CURRENT APPLICATION NUMBER: US/08/722.015A
; CURRENT FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-08-722-015A-19

Query Match 87.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCAGTCTAGCAGAAGAAG 22
:|||||:|||||
Db 1 TGGCAGTCTAGCAGAAGAAG 20

RESULT 10

US-08-470-202-25
; Sequence 25, Application US/08470202
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.202
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132.653

; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael J. Blake
; REGISTRATION NUMBER: 37,096
; REFERENCE/DOCKET NUMBER: 05495-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-470-202-25

Query Match 82.6%; Score 19; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGCAGTCTAGCAGAAGAAG 22
:|||||:|||||
Db 13 GGCAGTCTAGCAGAAGAAG 31

RESULT 11

US-08-471-770-25
; Sequence 25, Application US/08471770
; Patent No. 5770427
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/471.770
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132.653
; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 33 646.5

; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Carol P. Einaudi
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 05495-0001-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-471-770-25

Query Match 82.6%; Score 19; DB 1; Length 31;
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DB 13 GGCAGTCTAGCAGAGAAG 31

RESULT 12
US-08-468-059-25
; Sequence 25, Application US/08468059
; Patent No. 5840480
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; FILING DATE: 06-JUN-1995
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; FILING DATE: 05-OCT-1993
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; FILING DATE: 22-OCT-1992
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; ATTORNEY/AGENT INFORMATION:
; NAME: Carol P. Einaudi
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 05495-0001-02000
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; TELEPHONE: 202-408-4000
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US-08-468-059-25

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US-09-109-916-25
; Sequence 25, Application US/09109916
; Patent No. 6277561
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495,0001-04
; CURRENT APPLICATION NUMBER: US/09/109,916
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: DE P 42 33 646.5
; EARLIER FILING DATE: 1992-10-06
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; EARLIER FILING DATE: 1992-10-22
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; EARLIER FILING DATE: 1992-12-30
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; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-109-916-25

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DB 13 GGCAGTCTAGCAGAGAAG 31

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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442.731 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	23	100.0	23	6	AR131396	AR131396 Sequence
3	23	100.0	23	6	BD001801	BD001801 Immunogen
4	23	100.0	42	6	AR079771	AR079771 Sequence
5	23	100.0	42	6	AR081301	AR081301 Sequence
6	23	100.0	42	6	AR170661	AR170661 Sequence
7	22	95.7	22	6	AX210201	AX210201 Sequence
8	20	87.0	20	6	A46935	A46935 Sequence 19
9	20	87.0	20	6	AR082339	AR082339 Sequence
10	20	87.0	20	6	AR120881	AR120881 Sequence
11	20	87.0	20	6	AR207576	AR207576 Sequence
12	20	87.0	20	6	I78385	I78385 Sequence 18
13	19	82.6	20	6	E37099	E37099 Method for
14	19	82.6	20	6	E63428	E63428 Method for
15	19	82.6	31	6	A38018	A38018 Sequence 25
16	19	82.6	31	6	AR059442	AR059442 Sequence
17	19	82.6	31	6	AX001375	AX001375 Sequence
18	19	82.6	31	6	BD000304	BD000304 cDNA comp
19	17	73.9	30	6	I16038	I16038 Sequence 1
20	17	73.9	30	6	I16040	I16040 Sequence 3
21	17	73.9	30	6	I16814	I16814 Sequence 3
22	17	73.9	30	6	I36475	I36475 Sequence 2
23	17	73.9	30	6	I36477	I36477 Sequence 4
24	17	73.9	30	6	I63575	I63575 Sequence 3
25	15	65.2	33	6	AR105726	AR105726 Sequence
26	14	60.9	20	6	E63444	E63444 Method for
27	13	56.5	25	6	AR068041	AR068041 Sequence
28	13	56.5	46	6	I43893	I43893 Sequence 22
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30	12	52.2	24	6	AR159841	AR159841 Sequence
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33	12	52.2	44	6	A63250	A63250 Sequence 19
34	12	52.2	44	6	E31337	E31337 Process for
35	11	47.8	14	6	I28571	I28571 Sequence 24
36	11	47.8	14	6	I58733	I58733 Sequence 24
37	11	47.8	16	6	AR087169	AR087169 Sequence
38	11	47.8	16	6	AR150615	AR150615 Sequence
39	11	47.8	16	6	AR200489	AR200489 Sequence
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41	11	47.8	16	6	I42186	I42186 Sequence 21
42	11	47.8	16	6	I49624	I49624 Sequence 39
43	11	47.8	17	6	AR045799	AR045799 Sequence
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ALIGNMENTS

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LOCUS A31977 23 bp DNA linear PAT 08-JUL-1996
DEFINITION Synthetic HIV-1/2 diagnosis primer.
ACCESSION A31977
VERSION A31977.1 GI:1567260
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 23)
Moncany,M. and Montagnier,L.
Nucleotide sequences of retroviral genomes of types HIV-1, HIV-2
and HIV, their uses for the amplification of these genomes and
diagnosis in vitro of these viral infections

JOURNAL Patent: EP 0403333-A 32 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
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AR079771 42 bp DNA linear PAT 31-AUG-2000
LOCUS
DEFINITION Sequence 95 from patent US 5965726.
ACCESSION AR079771
VERSION AR079771.1 GI:10006512
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Pavlakis, G.N. and Felber, B.K.
TITLE Method of eliminating inhibitory/ instability regions of mRNA
JOURNAL Patent: US 5965726-A 95 12-OCT-1999;
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LOCUS
DEFINITION Sequence 95 from patent US 5972596.
ACCESSION AR081301
VERSION AR081301.1 GI:10008027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Pavlakis, G.N. and Felber, B.K.
TITLE Nucleic acid constructs containing HIV genes with mutated
inhibitory/instability regions and methods of using same
JOURNAL Patent: US 5972596-A 95 26-OCT-1999;
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JOURNAL Patent: EP 0403333-A 32 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
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AR131396 23 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 48 from patent US 6194142.
ACCESSION AR131396
VERSION AR131396.1 GI:14120299
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Moncany, M. and Montagnier, L.
TITLE Nucleotide sequences derived from the genome of retroviruses of the
HIV-1, HIV-2, and SIV type, and their uses in particular for the
amplification of the genomes of these retroviruses and for the in
vitro diagnosis of the diseases due to these viruses
JOURNAL Patent: US 6194142-A 48 27-FEB-2001;
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RESULT 3
BD001801 23 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
types.
ACCESSION BD001801
VERSION BD001801.1 GI:18626360
KEYWORDS JP 2000093187-A/48.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 23)
AUTHORS Moncany, M. and Montagnier, L.
TITLE Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
types
JOURNAL Patent: JP 2000093187-A 48 04-APR-2000;
COMMENT INST PASTEUR, INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL
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PN JP 2000093187-A/48
PD 04-APR-2000

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
TITLE Method and reagent for inhibiting human immunodeficiency virus replication
JOURNAL Patent: US 6159692-A 183 12-DEC-2000;
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LOCUS E37099 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for quantitating HIV-provirus DNA and diagnosis kit.
ACCESSION E37099
VERSION E37099.1 GI:18624781
KEYWORDS JP 2000157299-A/3.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kato,S., Hiraishi,Y. and Sugita,T.
TITLE Method for quantitating HIV-provirus DNA and diagnosis kit
JOURNAL Patent: JP 2000157299-A 3 13-JUN-2000;
COMMENT KEIO UNIV
 OS Artificial Sequence
 PN JP 2000157299-A/3
 PD 13-JUN-2000
 PF 30-NOV-1998 JP 1998340303
 PR
 PI SHINGO KATO,YOSHIYUKI HIRAISHI,TETSUYOSHI SUGITA PC
 C1201/70,C12N15/09,C12Q1/68,G01N33/50,G01N33/50/(C12Q1/70, PC
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LOCUS E63428 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for determining subtype of HIV-1.
ACCESSION E63428
VERSION E63428.1 GI:18633687
KEYWORDS JP 2001057891-A/4.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kato,S., Kobayashi,Y., Hiraishi,Y., Shimizu,K. and Sugita,T.
TITLE Method for determining subtype of HIV-1
JOURNAL Patent: JP 2001057891-A 4 06-MAR-2001;
COMMENT KEIO UNIV
 OS Artificial Sequence
 PN JP 2001057891-A/4

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
TITLE Method and reagent for inhibiting human immunodeficiency virus replication
JOURNAL Patent: US 6159692-A 183 12-DEC-2000;
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Db 1 TGGCAGTCTAGCAGAAG 20
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LOCUS AR207576 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from patent US 6379881.
ACCESSION AR207576
VERSION AR207576.1 GI:21507365
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fouchier,R.,Adrianus. and Schuitemaker,J.
TITLE Nucleic acids and methods for the discrimination between syncytium inducing and non syncytium inducing variants of the human immunodeficiency virus
JOURNAL Patent: US 6379881-A 19 30-APR-2002;
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LOCUS I78385 20 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 183 from patent US 5693535.
ACCESSION I78385
VERSION I78385.1 GI:3014539
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
TITLE HIV targeted ribozymes
JOURNAL Patent: US 5693535-A 183 02-DEC-1997;
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PD 06-MAR-2001
PF 01-FEB-2000 JP 2000023581
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PI SHINGO KATO, YOSHIO KOBAYASHI, YOSHIYUKI HIRAIISHI, KAYOKO
SHIMIZU,
PI TETSUYOSHI SUGITA
PC C12N15/09, C12Q1/68, C12Q1/70, G01N33/50, G01N33/569, C12N15/00 CC

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A38018
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DEFINITION Sequence 25 from Patent EP0591914.
ACCESSION A38018
VERSION A38018.1 GI:2294674
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Guertler J.G., Eberle, J.D., Brunn, V.A., Dr, Knapp, S.D. and
Hauser, H.D.
TITLE Retrovirus of the HIV-group and its application
JOURNAL Patent: EP 0591914-A 25 13-APR-1994;
COMMENT BEHRINGERWERKE AG (DE)
Other publication AU 4880093 940421
Other publication CA 2107732 940407
Other publication JP 6225760 940816
Other publication ZA 9307371 940429
Other publication DE 4235718 940428
Other publication DE 424541 940707
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Copyright (c) 1993 - 2002 Compugen Ltd.

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5	21	91.3	21	17	AAT42143
6	21	91.3	33	17	AAT42149
7	19	82.6	20	21	AAV72019
8	19	82.6	20	22	AAF26812
9	19	82.6	20	24	ABL50092

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
10	19	82.6	31	15	AAQ58949
11	19	82.6	31	20	AAQ22350
12	17	73.9	30	9	AAN80773
13	17	73.9	30	10	AAN92234
14	17	73.9	30	10	AAN92234
15	17	73.9	30	10	AAN92234
16	17	73.9	30	13	AAQ25361
17	17	73.9	30	13	AAQ25363
18	17	73.9	30	17	AAQ32899
19	17	73.9	30	18	AAV13873
20	17	73.9	30	18	AAV13873
21	17	73.9	30	18	AAV13873
22	17	73.9	30	18	AAV13873
23	17	73.9	30	18	AAV13873
24	14	60.9	20	22	AAF26828
25	14	60.9	20	24	ABL38128
26	14	60.9	20	24	ABL38128
27	14	60.9	39	16	AAQ81322
28	12	52.2	24	20	AAQ06932
29	12	52.2	24	21	AAA36911
30	12	52.2	24	21	AAA36911
31	12	52.2	24	21	AAA36911
32	12	52.2	24	21	AAA36911
33	12	52.2	24	21	AAA36911
34	12	52.2	25	21	AAZ61212
35	12	52.2	33	24	AAAL38084
36	12	52.2	34	21	AAAG2407
37	12	52.2	36	22	ABA01062
38	12	52.2	40	21	AAZ96035
39	12	52.2	42	20	AAV81541
40	12	52.2	42	21	AAV81541
41	12	52.2	44	20	AAV81542
42	12	52.2	44	20	AAV81542
43	12	52.2	44	21	AAV73059
44	12	52.2	45	22	AAF30747
45	12	52.2	48	16	AAQ84579
	12	52.2	49	21	AAQ99339

ALIGNMENTS

RESULT 1

AAQ06935

ID AAQ06935 standard; DNA; 23 BP.

XX

AC AAQ06935;

XX

DT 05-MAR-1991 (first entry)

XX

DE MY6 nucleotide constituent of env gene of HIV-1 Bru, HIV-1 Mal

DE and HIV-1 Eli.

XX

XX HIV-1; AIDS; sense nucleotide; ss.

XX

PN EP403333-A.

XX

PD 19-DEC-1990.

XX

PF 05-JUN-1990; 90EP-0401520.

XX

PR 20-SEP-1989; 89FR-0012371.

XX

PA (INSP) INST PASTEUR.

PA (INRM) INSERM INST NAT SANTE RE.

XX

PI Moncany M, Montagnier L;

XX

DR WPI; 1990-378039/51.

XX

PT New nucleotide sequences derived from genome of HIV-1, HIV-2 and

PT SIV - useful as primers for amplification of immuno-deficiency

PT viruses in diagnosis and for raising antibodies in treatment of

PT HIV infections

OS	Synthetic.
PN	FR2730493-A1.
XX	
PD	14-AUG-1996.
XX	
PF	09-FEB-1995; 95FR-0001513.
XX	
PR	09-FEB-1995; 95FR-0001513.
XX	
PA	(INSP) INST PASTEUR.
XX	
PI	Chamaret S, Cohen J, Guetard D, Montagnier L, Philbert F;
PI	Tabary T;
XX	
DR	WPI; 1996-395417/40.
XX	
PT	New HIV-1 strain MAD and related nucleic acids and peptide(s) -
PT	useful for diagnosing HIV-1 infections and generating vaccines
XX	
PS	Claim 24; Page 19; 24pp; French.
XX	
CC	A new strain of HIV-1 was isolated from a seropositive, asymptomatic
CC	woman from Zaire; her serum reacted only moderately with peptides
CC	specific for HIV-1, including subgroup O, and reacted with only one
CC	African-type V3 peptide. DNA fragments coding for the V3 loop of
CC	gp120 and gp41 from strain MAD were sequenced and analysed. Peptides
CC	derived from V3 loops of the new HIV-1 strain are useful in vaccines
CC	and for immunodiagnosis. The present sequence represents a claimed
CC	oligonucleotide primer for amplifying DNA coding for the V3 loop of
CC	HIV-1 strain MAD envelope glycoprotein gp120.
XX	
SQ	Sequence 21 BP; 9 A; 3 C; 6 G; 3 T; 0 other;
Query Match 91.3%; Score 21; DB 17; Length 21;	
Best Local Similarity 100.0%; Pred. No. 0.058;	
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 AATGGCAGTCTAGCAGAAGAA 21
Db	1 AATGGCAGTCTAGCAGAAGAA 21
RESULT 6	
AAT42149	
ID	AAT42149 standard; DNA; 33 BP.
XX	
AC	AAT42149;
XX	
DT	14-MAY-1997 (first entry)
XX	
DE	HIV-1 gp120 V3 loop PCR primer.
XX	
KW	Human immunodeficiency virus; HIV-1; envelope glycoprotein gp120;
KW	variable loop; zaire; acquired immune deficiency syndrome; AIDS;
KW	vaccine; immunodiagnosis; polymerase chain reaction; PCR; ss.
XX	
OS	Synthetic.
XX	
PN	FR2730493-A1.
XX	
PD	14-AUG-1996.
XX	
PF	09-FEB-1995; 95FR-0001513.
XX	
PR	09-FEB-1995; 95FR-0001513.
XX	
PA	(INSP) INST PASTEUR.
XX	
PI	Chamaret S, Cohen J, Guetard D, Montagnier L, Philbert F;
PI	Tabary T;
XX	
DR	WPI; 1996-395417/40.

XX New HIV-1 strain MAD and related nucleic acids and peptide(s) -
PT useful for diagnosing HIV-1 infections and generating vaccines
XX
PS Example; Page 12; 24pp; French.
XX
CC A new strain of HIV-1 was isolated from a seropositive, asymptomatic
CC woman from Zaïre; her serum reacted only moderately with peptides
CC specific for HIV-1, including subgroup O, and reacted with only one
CC African-type V3 peptide. Peptides derived from V3 loops of the new
CC HIV-1 strain are useful in vaccines and for immunodiagnosis. The
CC present sequence represents an oligonucleotide primer which was used
CC for amplifying DNA coding for the V3 loop of HIV-1 envelope
CC glycoprotein gp120 from various viral strains. A comparison of
CC different strains allowed the immunodominant epitope of HIV-1 MAD
CC to be identified.
XX
SQ Sequence 33 BP; 11 A; 7 C; 11 G; 4 T; 0 other;

Query Match 91.3%; Score 21; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCAGTCTAGCAGAAG 21
DB 13 AATGGCAGTCTAGCAGAAG 33
|||||

RESULT 7
AA72019
ID AAA72019 standard; DNA; 20 BP.
XX
AC AAA72019;
XX
DT 20-NOV-2000 (first entry)
XX
DE HIV-1 proviral DNA inner PCR primer, SEQ ID NO:3.
XX
KW HIV-1 proviral DNA; quantitative analysis; competitive nested PCR;
KW diagnostic marker; inner PCR primer; ss.
XX
OS Human immunodeficiency virus type 1.
XX
PN JP2000157299-A.
XX
PD 13-JUN-2000.
XX
PF 30-NOV-1998; 98JP-0340303.
XX
PR 30-NOV-1998; 98JP-0340303.
XX
PA (KEIO-) GH KEIO GIJUKU.
XX
DR WPI; 2000-468210/41.
XX
PT A method and a diagnosis kit for quantitative analysis of HIV-1
PT provirus DNA -
XX
PS Example 1; Page 4; 11pp; Japanese.
XX
CC The invention relates to a method and diagnostic kit for the
CC quantitative analysis of HIV-1 provirus DNA, and to a marker for the
CC effective treatment of anti-HIV-1 therapy. The method and kit of the
CC invention can be used for the evaluation of progress of HIV-1 related
CC diseases and/or efficacy of anti-HIV-1 therapy. The invention discloses
CC a method for amplification of a specific site within HIV-1 provirus DNA
CC comprising annealing a primer which is partially complementary to HIV-1
CC provirus DNA and performing an amplification reaction in which the
CC reaction mixture is incubated at 48+/-4 degrees Celsius and then 64+/-4
CC degrees Celsius at least once for each step. This is performed in the
CC presence of a known amount of competitor DNA, and the amplified HIV-1
CC proviral DNA is isolated and quantified. The invention provides effective
CC means for the diagnosis and staging of HIV-1 infection, and for the

CC evaluation of the efficacy of anti-HIV-1 treatment. Sequences AAA72017-
CC AAA72027 represent HIV-1 PCR primers used in the method of the
CC invention. Sequences AAA72019-A72020 are outer primers used in
CC competitive nested PCR in an exemplification of the invention.
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

Query Match 82.6%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCAGTCTAGCAGAAG 19
DB 2 AATGGCAGTCTAGCAGAAG 20
|||||

RESULT 8
AAF26812
ID AAF26812 standard; DNA; 20 BP.
XX
AC AAF26812;
XX
DT 05-APR-2001 (first entry)
XX
DE HIV-1 subtype determining PCR primer SEQ ID NO:4.
XX
KW HIV-1; subtype; human immunodeficiency virus; detection; PCR primer;
KW characterisation; env; envelope; ss.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200077219-A1.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-JP03896.
XX
PR 15-JUN-1999; 99JP-0167736.
PR 01-FEB-2000; 2000JP-0023581.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
PA (UYKE-) UNIV KEIO.
XX
PI Kato S, Kobayashi Y, Hiraishi Y, Shimizu K, Sugita T;
XX WPI; 2001-168279/17.
XX
DR Determining the subtype of human immunodeficiency virus (HIV)-1,
PT comprises nucleic acid amplification of the termini of the HIV-1 env
PT (envelope) gene -
XX
PS Claim 13; Page 33; 63pp; Japanese.
XX
CC The present invention describes a method for determining the subtype of
CC human immunodeficiency virus (HIV-1). The method comprises: (a) nucleic
CC acid amplification of the 5' terminal and/or 3' terminal of the
CC nucleotide sequence of the HIV-1 env (envelope) gene, which differs
CC according to the sub-type, as a target sequence; and (b) detecting
CC whether or not the target sequence is present. The method is used to
CC determine a subtype of human immunodeficiency virus (HIV-1). AAF26809 to
CC AAF26842 represent PCR primers used in the exemplification of the method.
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

Query Match 82.6%; Score 19; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCAGTCTAGCAGAAG 19
DB 2 AATGGCAGTCTAGCAGAAG 20
|||||

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RESULT 9
ABL50092
ID ABL50092 standard; DNA; 20 BP.
XX
AC ABL50092;
XX
DT 11-JUN-2002 (first entry)
XX
DE HIV-1 env gene detection PCR primer 10 SEQ ID NO:4.
XX
KW Human immunodeficiency virus; HIV-1; detection; env; PCR primer; ss.
XX
OS Human immunodeficiency virus type 1.
XX
PN JP2002000277-A.
XX
PD 08-JAN-2002.
XX
PF 28-JUN-2000; 2000JP-0194968.
XX
PR 28-JUN-2000; 2000JP-0194968.
XX
PA (KEIO-) GH KEIO GIJUKU.
XX
DR WPI; 2002-298282/34.
XX
PT Detection of HIV-1 comprises amplification using the nucleotide
sequence of the env gene of HIV-1 as the target -
XX
PS Disclosure; Page 5; 20pp; Japanese.
XX
CC The present invention describes a method for detecting HIV-1. The method
comprises an amplification reaction using part of the nucleotide
sequence of the HIV-1 env gene as the target sequence and confirming
the presence or the absence of HIV-1 by the presence this sequence. The
sequence is highly conserved between a number of subtypes. The present
invention also describes: (1) a primer which is part of the nucleotide
sequence of env gene of HIV-1; and (2) a kit for detecting HIV-1
comprising a primer pair. The present sequence represents a PCR primer
for the HIV-1 env gene which is used in the exemplification of the
present invention.
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

Query Match      82.6%; Score 19; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCAGTCTAGCAGAAG 19
   |||||
DB 2 AATGGCAGTCTAGCAGAAG 20

RESULT 10
AAQ58949
ID AAQ58949 standard; DNA; 31 BP.
XX
AC AAQ58949;
XX
DT 04-NOV-1994 (first entry)
XX
DE 5v3deg1 primer.
XX
KW Human immunodeficiency virus; HIV; antigen; detection; diagnosis;
retrovirus; vaccine; lymphocyte; reverse transcriptase;
KW amplification; primer; polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP591914-A.
XX
PD 13-APR-1994.
XX

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PF 05-OCT-1993; 93EP-0116058.
XX
PR 06-OCT-1992; 92DE-4233646.
XX
PR 22-OCT-1992; 92DE-4235718.
XX
PR 30-DEC-1992; 92DE-4244541.
XX
PR 01-JUN-1993; 93DE-4318186.
XX
PA (BEHW ) BEHRINGWERKE AG.
XX
PI Brunn VA, Eberle J, Gurtler LG, Hauser H-P, Knapp S;
XX
DR WPI; 1994-120077/15.
XX
PT New HIV-type immune deficiency virus ECACC V 92092318 - and
deriv. cDNA or antigens, useful for diagnosing retroviral
PT infections and vaccines
XX
PS Disclosure; Page 5; 73pp; German.
XX
CC MVP-5180/91 DNA is obtained by PCR using the primers given
in AAQ58925-958.
XX
SQ Sequence 31 BP; 10 A; 6 C; 10 G; 5 T; 0 other;

Query Match      82.6%; Score 19; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCAGTCTAGCAGAAGAAG 22
   |||||
DB 13 GGCAGTCTAGCAGAAGAAG 31

RESULT 11
AAQ22350
ID AAX22350 standard; DNA; 31 BP.
XX
AC AAX22350;
XX
DT 19-MAY-1999 (first entry)
XX
DE HIV-1 PCR primer 5v3deg1.
XX
KW HIV-type retrovirus; MVP-5180/91; ECACC V 92092318; antigen; assay kit;
KW detection; antibody; immune deficiency; vaccine; PCR primer; ss.
XX
OS Synthetic.
XX
OS Human immunodeficiency virus type 1.
XX
PN EP890642-A2.
XX
PD 13-JAN-1999.
XX
PF 05-OCT-1993; 93EP-0116058.
XX
PR 01-JUN-1993; 93DE-4318186.
XX
PR 06-OCT-1992; 92DE-4233646.
XX
PR 22-OCT-1992; 92DE-4235718.
XX
PR 30-DEC-1992; 92DE-4244541.
XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
PI Brunn AV, Eberle J, Gurtler LG, Hauser H, Knapp S;
XX
DR WPI; 1999-072878/07.
XX
PT New HIV-type retrovirus and corresponding cDNA, recombinant DNA and
antigen - used for detecting retro-viruses that cause immune
PT deficiency and to prepare vaccines
XX
PS Disclosure; Page 4; 39pp; German.
XX
CC This invention describes the isolation of a novel HIV-type retrovirus

```

CC called MVP-5180/91 (ECACC V 92092318). Antigens produced from this
 CC product can be used in an assay kit for detecting antibodies against
 CC viruses that cause immune deficiency, preferably where the assay is a
 CC Western blot, ELISA or fluorescence immunoassay. MVP-5180/91, cDNA
 CC and/or antigen can be used for detecting retroviruses that cause immune
 CC deficiency and to prepare vaccines. This sequence represents a PCR primer
 CC used in the method of the invention.

XX Sequence 31 BP; 10 A; 6 C; 10 G; 5 T; 0 other;

Query Match 82.6%; Score 19; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCAGTCTAGCAGAAGAAG 22
 |||||
 DB 13 GGCAGTCTAGCAGAAGAAG 31

RESULT 12

AAN80773/c
 ID AAN80773 standard; DNA; 30 BP.

XX
 AC AAN80773;

DT 03-OCT-2002 (updated)
 DT 16-OCT-1990 (first entry)

XX Probe for detection of HIV-1.

DE Human immunodeficiency virus-1; ss.

XX
 OS Homo sapiens.
 OS Synthetic.

XX
 PN WO8801302-A.

XX PD 25-FEB-1988.

PF 11-AUG-1987; 87WO-US01966.

PR 11-AUG-1986; 86US-0895756.

XX (SISK-) SISK DIAGNOSTICS I.

XX Gingeras TR, Ghosh SS, Davis GR, Kwoh DY, Musso GF;

XX WPI; 1988-064017/09.

XX Nuc. acid probe assay - using a probe which is end-attached to a support
 PT and a labelled probe with a sequence non complementary to the 1st probe

XX Claim 16; Page 51; 55pp; English.

XX This probe can alternatively be RNA and is used in an assay for HIV-1.
 CC (Updated on 03-OCT-2002 to add missing OS field.)

XX Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;

Query Match 73.9%; Score 17; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGTCTAGCAGAAGAAGA 23
 |||||
 DB 30 AGTCTAGCAGAAGAAGA 14

RESULT 13

AAN92234/c
 ID AAN92234 standard; DNA; 30 BP.

XX
 AC AAN92234;

XX 14-FEB-1990 (first entry)
 DT Probe for HIV-1 virus.
 DE Lanthanide chelate-tagged probe; HIV-1 virus; human immunodeficiency
 KW virus.
 KW Human immunodeficiency virus 1 (HIV-1).

XX WO8904375-A.

XX 18-MAY-1989.

XX 21-OCT-1988; 88WO-US03735.

XX 23-OCT-1987; 87US-0112855.

XX (SISK-) SISK DIAGNOSTICS I.

XX Musso GF, Ghosh SS, Gingeras TR;

XX WPI; 1989-165653/22.

XX Lanthanide chelate-tagged nucleic acid probes
 PT - used in hybridisation assays with high sensitivity
 PT due to intense fluorescence of the ions

XX Example II (B); page 61; 94pp; English.

XX Probe for HIV-1 virus. It can be derivatized at the 5'- and 3'-terminal.

XX Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;

Query Match 73.9%; Score 17; DB 10; Length 30;

Best Local Similarity 100.0%; Pred. No. 7;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGTCTAGCAGAAGAAGA 23

DB 30 AGTCTAGCAGAAGAAGA 14

RESULT 14

AAN94510/c
 ID AAN94510 standard; DNA; 30 BP.

XX
 AC AAN94510;

XX 28-JUN-1990 (first entry)

XX Primer used to target HIV-1 virus allows for it's rapid duplication.

XX Polymerase extension; gene amplification; PCR; HIV-1; AIDS; ds.

XX Synthetic.

XX WO8810315-A.

XX 29-DEC-1988.

XX 17-JUN-1988; 88WO-US02108.

XX 19-JUN-1987; 87US-0064141.

XX 06-JUN-1988; 88US-0202978.

XX (SISK-) SISK DIAGNOSTICS INC.

XX Gingeras TR, Merten U, Kwoh DY;

XX WPI; 1989-023856/03.

XX Transcription-based nucleic acid amplification -

PT using nucleic acid primers corresp. to a segment of a target
PT sequence and a polymerase extension.
XX
PS Claim 48; Page 74; 86pp; English.
XX
CC 3'-Primer subsegment 1 in the presence of a polymerase, enables
CC amplification of a sequence within the genome of HIV-1.
XX
SQ Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;

Query Match 73.9%; Score 17; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGTCTAGCAGAGAAGA 23
DB 30 AGTCTAGCAGAGAAGA 14

RESULT 15
AAQ25361/c
ID AAQ25361 standard; DNA; 30 BP.
XX
AC AAQ25361;
XX
DT 21-NOV-1992 (first entry)
XX
DE Sequence of detection oligonucleotide 86-272 for HIV-1 envelope
DE region.
XX
KW Detection probe; capture probe; primer; HIV-1 envelope protein;
KW hybridisation; ss.
XX
OS Synthetic.
XX
PN W09208808-A.
XX
PD 29-MAY-1992.
XX
PF 14-NOV-1991; 91WO-US08523.
XX
PR 14-NOV-1990; 90US-0613174.
XX
PA (SISK-) SISK DIAGNOSTICS INC.
XX
PI Ghosh S, Ishii JK;
XX
DR WPI; 1992-200192/24.
XX
PT Detecting single-stranded target nucleic acid - by hybridisation
PT to oligo:nucleotide(s) bonded to polystyrene support and
PT detection with oligo:nucleotide(s)
XX
PS Example, Page 24; 56pp; English.
XX
CC The inventors claim a method for detecting a single-stranded (ss)
CC target nucleic acid (T) by hybridisation to a detection
CC oligonucleotide (dON) bonded to a polystyrene support followed by
CC hybridisation with a capture ON (cON). dON 86-272 (ID 1) is based on
CC the Ratner S06620-6591 of the HIV-1 envelope region RNA
CC transcript. The cON 88-297 (ID 2) is based on the Ratner SQ 6560-6531.
CC The T for this pair of ONs is a 32p labeled 218 base HIV-1 envelope
CC region RNA transcript defining 6661 to 6450 region of the Ratner
CC sequence.
XX
SQ Sequence 30 BP; 6 A; 9 C; 2 G; 13 T; 0 other;

Query Match 73.9%; Score 17; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGTCTAGCAGAGAAGA 23
DB 30 AGTCTAGCAGAGAAGA 14

Db 30 AGTCTAGCAGAGAAGA 14

Search completed: December 5, 2002, 23:00:20
Job time : 206.592 secs

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